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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 17:50:45 ; Search time 8647.11 Seconds
(without alignments)
11250.449 Million cell updates/sec

Title: US-09-646-224A-1

Perfect score: 5897
Sequence: 1 ggaagccatcacgtgcccctga.....gaaaaaaaaaaaaaaaaaaaaa 5897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.cm.*
- 5: gb.ov.*
- 6: gb.pat.*
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- 34: em.htg_inv.*
- 35: em.htg_rod.*
- 36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	5897	100.0	5897	6	AX017217 Sequence
2	5882.6	99.8	5905	10	AF059030 Rattus no
3	5834.6	98.9	5849	10	AJ237852 Rattus no
4	5822.4	98.7	5908	6	E36122 Nucleic aci
5	5295.6	89.8	5334	6	E36125 Nucleic aci
6	4634.2	78.6	5858	10	AF118044 Mus muscu
7	4616.6	78.3	5921	10	AB031389 Mus muscu
8	3242.6	55.0	6237	9	AF188679 Homo sapi
9	3234.2	54.8	6528	9	AF109737 Homo sapi
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ALIGNMENTS

RESULT 1

AX017217	LOCUS	AX017217	5897 bp	DNA	PAT	07-SEP-2000
AX017217	DEFINITION	Sequence 1 from Patent WO9947670.				
AX017217	ACCESSION	AX017217				
AX017217.1	VERSION	AX017217.1	GI:10042137			

KEYWORDS
Norway rat.
Rattus norvegicus

ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 5897)
Tate,S.N., Grose,D.T. and Hick,C.A.

AUTHORS
Mammalian sodium channel proteins

TITLE
Patent: WO 9947670-A 1 23-SEP-1999;

JOURNAL
TATE SIMON NICHOLAS (GB); GLAXO GROUP LTD (GB); GROSE DAVID THOMAS (GB); HICK CAROLINE ANNE (GB)

FEATURES
Location/Qualifiers
1. .5897

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Db 3669 TACCGAAGTTCCGAACCGAAGCCAATGTACATTTAGTAATTTACTCGTGAAGAGTCCCGCA 3728
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Qy	5019	cgaccgctccatgcatggatgtctctcttctcttccactaccagggctctccgcggagactc	5078
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Qy	5139	taagaagctctacagcccatagtcacacacacgaaggaagagagaggaagcagcgc	5198
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Qy	5199	cgccgtcatcagagggcctaccggaaacacatgagagaagatggctcaaaactgagcgtgaa	5258
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DEFINITION	Nucleic acid encoding sodium channel of nerve tissue.		
ACCESSION	E36125		PAT 07-FEB-2001
VERSION	E36125.1	GI:13022508	
KEYWORDS	JP 199235186-A/4.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 5334)		
AUTHORS	Paul,S.D.L.L., Fish,R.K.D.D., Rambert and Laksmi,S.		
TITLE	Nucleic acid encoding sodium channel of nerve tissue		
JOURNAL	Patent: JP 199235186-A 4 31-AUG-1999;		
COMMENT	F HOFFMANN LA ROCHE AG OS Artificial Sequence PN JP 199235186-A/4 PD 31-AUG-1999 PP 20-NOV-1998 JP 1998331769 PR 20-NOV-1997 US 60/066225 PI PAUL SHATUA DAITORICHI,LINDA MARIE FISH,RINA KEIRU, PI DOUGLAS KENESU RAMBERT, PI LAKSMI SANGEIMUSUWARAN PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12N15/02,C12P21/02,PC C12P21/08, C12P21/08, PC C12Q1/68,G01N33/53,G01N33/577,G01N33/68//C12N5/10,C12R1/91), PC (C12P21/02,C12R1/91),(C12P21/08,C12R1/91),C12N15/00,C12N5/00, PC C12N15/00, CC (C12N5/00,C12R1/91) CC CC FH Key Location/Qualifiers FT source 1..5334 /organism='Artificial Sequence'. FEATURES source Location/Qualifiers 1..5334 /organism="unidentified" /db_xref="taxon:32644" BASE COUNT 1300 a 1338 c 1314 g 1382 t ORIGIN		
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		Best Local Similarity 99.7%; Pred. No. 0;	
		Matches 5304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	
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Db	14	CAGGTGAAGATGGAGGAGGAGGTACTACCGGTGATCTCCCGACGACGCGGAATTCG	73
Qy	99	cccttcacttcgactctcgtgcataaagaacgagcggtgtctatcccaaaaggagag	158
Db	74	CCCTTCTACTTCCGACTCTCTGGTGCCTATAGAGAAGCGGATGTGATCTCAAAAGGAGAG	133
Qy	159	gaagaagtcctcaagaacaggcgagctgagcccccagcctcggcctcagcttgacctaaa	218
Db	134	GAAGAAGTCCCAAGACAAGCGGCGAGCTGAGCCCCAGCTCGGCTCAGCTTGACCTAAA	193
Qy	219	ggctcccgaggagttaccctaaagctttatggtagacttccccctgagctgtgtacgaacc	278
Db	194	GGCTCCAGGAAGTTACCTAAGCTTTATGGTGACATTCCTCCCTGAGCTTGTAGCGAAGCC	253
Qy	279	tctggagacctgacccctactcaaaagaccataagacattcatcgtgttgaaacaagaa	338
Db	254	TCTGAAGACCTGGACCCATTCTACAAAGACCAATGAAGACATTTCATGGTGTGAACAAGAA	313

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DB 314 GAGAACAAATTTATCGCTTCAGCGCAAGCGGCTTGTTCATTCCTGGGCTTTTAATCC 373
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DB 374 CTTGAGAGCTTAATGATTCGTATCTCTGTCATTTCAGTCTTTAGCATGTTTCATCATCTG 433
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BASE COUNT 1530 a 1447 c 1396 g 1548 t
ORIGIN

Query Match 78.3%; Score 4616.6; DB 10; Length 5921;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 5183; Conservative 0; Mismatches 614; Indels 78; Gaps 12;

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AUTHORS Dib-Hajj, S.D., Tyrrell, L., Cummins, T.R., Black, J.A., Wood, P.M. and
Waxman, S.G.
TITLE Two tetrodotoxin-resistant sodium channels in human dorsal root
ganglion neurons
JOURNAL FEBS Lett. 462 (1-2), 117-120 (1999)
MEDLINE 20047838
REFERENCE 2 (bases 1 to 6237)
AUTHORS Dib-Hajj, S.D., Tyrrell, L., Cummins, T.R., Black, J.A. and Waxman, S.G.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A,
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RESULT 9

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LOCUS
DEFINITION
(SCN12A) mRNA, complete cds.
ACCESSION
AF109737
AF109737 6528 bp mRNA
Homo sapiens voltage-gated sodium channel alpha subunit SCN12A
PRI
15-JAN-2000

QY 5410 ggcag 5414
 Db 5639 GTCAG 5643

RESULT 10

AF150882

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

BASE COUNT

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1199 g

1650 t

1 others

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10

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AF150882 5728 bp mRNA PRI 15-JAN-2000
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 splice variant SCN12A-s (SCN12A) mRNA, complete cds.
 AF150882
 AF150882.1 GI:6693704
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 5728)
 Jeong, S.-Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N.,
 Hirai, M., Isahara, K., Uchiyama, F., and Kanazawa, I.
 Identification of a novel human voltage-gated sodium channel alpha
 subunit gene, SCN12A
 Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
 2 (bases 1 to 5728)
 Jeong, S.-Y., Suzuki, T., Hashida, H., Ogata, K., Masuda, M., Goto, J.,
 and Kanazawa, I.
 Direct Submission
 Submitted (12-MAY-1999) Neurology, Graduate School of Medicine,
 Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan
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ORIGIN

Query Match 43.8%; Score 2585.6; DB 9; Length 5728;
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Qy 2005 tacaacacatgtctgataacaataggtcttcttcttggcttccctcagagtgctgaggtc 2064
Db 2171 AACTGTGTACTTCAAAAGAGAAAGCTGGCCATCTTCTGGTTCCTTTCAGGGTCTCAGGGTC 2230
Qy 2065 tcaagttagcacaactcctggccacagttaaacactctcttaagatcatcggccactcc 2124
Db 2231 TTCAAGTTAGCCAAATCTTGGCCAACTTTGAACACACACTTAATTAAGATAAATCGGCAACTCT 2290

Qy 2125 gtgggagcgtctgaaacctgactgtgggtcctgactatcgtggtcttcactctttctgtg 2184
Db 2291 GTCGGAGCCCTTGAAACCTTGACTGTGCTCTGCTGATCTTAATTTCTCAGTA 2350
Qy 2185 gtgggagcgtcgtcttccggcaccagttaa--caagaccgctcagccaccagagc 2242
Db 2351 GTTGGCATGACGCTTTTGGCCGTAGCTCAATTTCCAAAAGAGTCCAAAACCTGTGTAAC 2410
Qy 2243 ggccag--cggcgtcggcacatggataattttctaccactcc 2283
Db 2411 CCACAGCCCGCAGACGTCTCATGTTTACGCACTGGGCACATGGGGATTTCTGGCACTCC 2470
Qy 2284 ttctggtggtgttcocgactcctctgtggtggaatggatcgagaacaatggtgggtgcag 2343
Db 2471 TTCTTAGTGTATTTCCGCATCTCTGCGGGAATGGATCGAAAATATGTGGGAATGTATG 2530
Qy 2344 caagataagacggtccccc--ttgtgcatcattgtcttcttctcgataaaggtgac 2400
Db 2531 CAAGAAGCAATGCATCATCATTTGTGTTATTGCTTTCATATTTGATCACGGTGATA 2590
Qy 2401 ggaagcttgggtgttaacctcttcattgcttgcctgctcaattcttcacgcaatgag 2460
Db 2591 GGAACACTTGTGTGCTCAACCTCTTCAATTCCTTACTGCTCAATTCCTTTAGCAATGAG 2650
Qy 2461 gagaagatgggagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 2520
Db 2651 GAAAGAAATGAAACTTTAGAGGAGAGGCCAGGAAAACCTAAAGTCCAGTTAGCACTGGAT 2710
Qy 2521 cgggtccgcgggctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 2580
Db 2711 CGATTCCGCGCGGCTTTTGTGTTGTGAGACACACTCTTGTGAGCATTTCTGTCAACAGTGG 2770
Qy 2581 tgagaggaagaaactcgcacaaagacaaagagacacagaaagcttctgctgggagaaat 2640
Db 2771 TGAGGAGGACAAACCTTACCACAGCAAAAGAGGTGCGCAGGAGGCTGTGCTGCACAAGC 2830
Qy 2641 aaagactcaatctcccggtgcgagggcctcctcctcctcctcctcctcctcctcctcctcct 2687
Db 2831 AAAGACATCATTCCTCCCTGGTGCATGGAGATGAAAGGGGCTCAGAGACCCAGGAGGAGCTT 2890
Qy 2688 -----agacatggttctacactggacagccggggtcctcctcctcctcctcctcctcctcct 2730
Db 2891 GGTATAACCTCTGTACCAAGACCTCTGGGCTCAGGCGATGATTTGGATTTGGTGGCA 2950
Qy 2731 ccactcgcagaggtagagcagatgtggaatatgttgatgaagcgtgcctaccaccc 2790
Db 2951 CCACCTCGGAGGAGGAGATGACGTTGAATTTCTGTTGAAGATATATGACACGGCATC 3010
Qy 2791 tcacaacatagtgctggagttcagcggtgacctcctcctcctcctcctcctcctcctcctcctcct 2850
Db 3011 ACACAACCTGAGCCTGAACAACAGCCCTATGAGCTCCATCAGGAGAACAAAGAACCCACG 3070
Qy 2851 agcccgaatgaccaaggggttgaaatggaagtatttcttgaagaagatctgcatattagc 2910
Db 3071 AGCCAGAGAGTTCAAGTGTGGAATTTGACATGTTCTCTGAAGATGAGCCTCATCTGACC 3130
Qy 2911 atacagagtcctcgaaagaagtcagcagtagagatgctcctcggaatcgagcacaatt 2970
Db 3131 ATACAGGATCCCCGAAAGAGTCTGATGTTACCAGTATACTATATCAGAAATGTAGCACCATT 3190
Qy 2971 gacctgaatgatacttcttagaaatttacagaaaaacagtttcccccaaaaaagcagccagat 3030
Db 3191 GATCTCAGGATGGCTTTGGATGGTTACCTCAGATGGTT---CCCAAAAACCAACACAGAG 3247
Qy 3031 agatgctttcccaagggccttagttgtoactttctatgcccacaaacacagacagagaaag 3090
Db 3248 AGATGTTGCCCCAAAGGCTTTGTTGCTGCTTCCATGCTGTAGCTGTGAGCAAGAGAAAG 3307
Qy 3091 tccccctgggtcgtctgtggtggaacattcggaaaaacctgtaccaaaatcggtgaagcacagc 3150
Db 3308 CCTCCCTGGGTCAATTTGGTGGAACTCGGAAAAACCTGCTACCAAAATAGTGAAACACAGC 3367

IVSIFGNSFAYVKESGIDDMFETFGNSIICLFETTSAGWDGLLNPIILNSPPD
CPNLENPTSVKGCNPSIGCFPCSYIIISFLIVNMYTAILLENFNVAEESSE
PIGEDFNFYETWEFDATQFIAYSRLSDFTDLOEPLRIAKNPKIKLITLDLPM
VPDKTHCLDILFALTKEVLGSDGEMDALKOTMEKFAANPSKVSYEYITITLKRKH
EVCATKIORAYRRHLLORSMKOASMYRSHSDGSDDAPEKEGLLANTMSKMYGHEN
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/gene="SKM1"
5889..7823

3' UTR
BASE COUNT 1621 a 2354 c 2147 g 1701 t
ORIGIN Chromosome 17q23.1-25.3.

Query Match 24.0%; Score 1414.2; DB 9; Length 7823;
Best Local Similarity 57.6%; Pred. No. 0;
Matches 3007; Conservative 0; Mismatches 2093; Indels 117; Gaps 22;

QY	94	ttccgcccccttcctccgactctggtgctgccataaagaagcgattgctatcccaaaag	153
DB	126	TTGGCGCCCTTCACCCGGGAGTCACCTGGCAGCCATGAACAGCGGGCGGTGGAGGAGG	185
QY	154	g---agagggaaggtccaaagacaagcgcgagctgagccccagcctcgccctcagctt	210
DB	186	GCCCGGCTGCAGCGGAATAAGCAGATGAGATTGAGGAGCCCGAACGACCCACGAGT	245
QY	211	gaactaaagcctccaggaagttacctaagctttatggtgacattccccctgagctgtt	270
DB	246	GACTTGGAGGCTGCAAGAACCTTACCATGATCTACGAGACCCCGCGGGAGGTATC	305
QY	271	acgaacctctggaggaacctggaccctactataaagaaccataagaacattcaggtgtg	330
DB	306	GGCATCCCTCTGGAGGACCTTGGATCCCTACTACAGCAATAAGAAAGACCTTTCATCGTACTC	365
QY	331	aacaagaagaacaatttatcttcagcgcaagcgccctgttcttcattctggggcct	390
DB	366	AACAAGGCAAGGCCATCTTCCGCTTCTCCGCCACACCTGCTCTCTACCTGCTGAGCCCC	425
QY	391	tttaatccccctcagaagcttaagtattctctgcttccattcagctctttagcatgtc	450
DB	426	TTGAGCTAGTCAGGCGCGGGGCATCAAGGTGCTATCCTATCCATGCGCTGTTTCAGCATGTC	485
QY	451	atcatctgcaggtgatcaactgatatgttcatggcggaattctatggagagaagtttc	510
DB	486	ATCATGATACCACTTCTTGACCAACTGCGTATTATGATGACCA---TGAGTGACCCGCCCTCCC	542
QY	511	gacaacgacattccgaatacgtcttcattgggatttatatttagagctgtgattaaa	570
DB	543	TGGTCCAAGATGTGGAGTACACCTTCACAGGNTCTACACCTTTGAGTCCCTCATCAAG	602
QY	571	atattgggaaggtcttcattgttgatgttttctctccagagatccggtgaaactgg	630
DB	603	ATACTGGCCGAGGCTTCTGTGTCGAGACTTCACATTCCTCGGGACCCCTGGAACCTGG	662
QY	631	ctggactctattgattggaacagcagatgcgaactgttttccggcgagcccaagtaaat	690
DB	663	CTGGACTTCACTGATGATGAGGCTGCTGAGAGTTCACAGAGTTTGTGG---ACTTGGGGAAC	719
QY	691	ctttcagctcttcgtatctccagtggttcagagctctgaagcgatttcagttatctca	750
DB	720	ATCTACGCTTGAGGACCTTCCGGGTGCTCGGGGCCCTCAAAACCATCAGCGGTATCCCA	779
QY	751	ggtctgaaggtcatcgtagtgccctgctgctgcgtcggtgaagagctggttagcgtgatg	810
DB	780	GGGCTGAAGACGATCGTGGGGGCCCTGATCCAGTCCGTGGAAGAGCTGTCGGATGTGATG	839
QY	811	gtcctcaactctctcagcatctttggcctggtcggttcagcagcgtgttcattggga	870
DB	840	ATCCTCACTCTCTCTGCTGAGCGCTTTTGGCTGGTAGGACTTGCAGCTCTTCATGGGA	899
QY	871	attctgaaccagagtgatat---taagcacaactgtgtggcccccaacctgcatccaaag	927
DB	900	AACCTGAGGAGAAAGTGTGTGCGCTGGCCCCCGCGCTTCAACGACACCAACACCGCTGG	959
QY	928	gattgcttgaagaggaagaaagatagcgaagacttcaataatgtgtgtaacctggtgcgcg	987

DB	960	TACAGCAATCACAGCTGGTACGGCAATGACACATGGTATGGCAATGAGATGTGGTACGCG	1019
QY	988	a---gagacctgtcccaatggtctcactgctgataaaacacattgaacccagacaat	1044
DB	1020	ANTGACTCATGGTATGCCAACACACAGCTGGAACAGCCATGCAAGCTGGGCCACCAACAT	1079
QY	1045	aatatacaaaagtttgacaactttggctgtccctttctcgcctatgttcccggttatgaact	1104
DB	1080	ACCTTTGATTGGGACGCTTACATCAGTGATGAAGGAACCTTCTACTTCTCTGGAGGGCTCC	1139
QY	1105	caagactcctgggagaggttttaccg--acagatcctcgcgac--cctcgggatactactt	1161
DB	1140	AACGATCCCTGCTCTGTGGGAACAGCAGTATCTTCTGTGGCAGCTGCCCCTAAGGGTTATGAG	1199
QY	1162	gtctctctctgtgtgtgtcactctcctgtggtccctctcactcgtttaaactaaacctg	1221
DB	1200	TGANTCAAGACCGGGCGGAACCCCACTATGGCTTACACAGCTATGACACTTTCAGCTGG	1259
QY	1222	gc--tgtgtcaccatggcttatgaagaacacagaaatgttagctgctgagacagag	1279
DB	1260	GCCTTCTGTGCTCTCTTCCGCTCATGACACAGGACTATTGGGAGAACCTCTTCCAGCTG	1319
QY	1280	ccaaggagaataatgttccaggaagcccgagctgtgttaaaggagagaa-----ggagggc	1334
DB	1320	ACCTTTCGAGCAGCTGGCAAGACCTACATGATCTTCTTCTGTGTCATCATCTTCTCTGGGC	1379
QY	1335	tcgtgttgccatgggaattgacagaagtcccttaattccctcaagctcactccttttc	1394
DB	1380	TCCTTTCATCTCAATCTGATCTCTGGCGCTGGTGGCCATGGCATATGGCGAGCAGAA	1439
QY	1395	ccgaagaagaggaagttttccgtagtaagacaagaagtccttc--tttatgagaggg	1452
DB	1440	GAGGCCACCTTGGCCGAGGATAAGGAGAAAGAGGAGGAGTTTCAGCAGATGCTTGAAGAAG	1499
QY	1453	tccaagcggcccaagcctcagcgtctgatttcagagagcagtgctccttaaaaaatccacag	1512
DB	1500	TTCAAAAAGCACCAGGAGGAGCTGGAGAAGGCCAAGGCCGCCAAGCTCTGGAAGGTGGG	1559
QY	1513	ctccttgagcagacccaacagactgtccagaaactgccaagtgcagatctctttagagacab	1572
DB	1560	GAGCAGATGGGGACCCAGCCCATATGGCAAACTGCAATGGCAGCCTGGACACATCCGAA	1619
QY	1573	gtgagccccctccacagcgagagagcgtgagcgtctcagtactttaaccatcaccata	1632
DB	1620	GGGAGAAGGAGGCCCGAGGAGCGGCGGAGCAGCGGCATCTCCGACGCCCATG	1679
QY	1633	caggacaagaataatccagggagcctgtttcccatgtgggaaaaaatttggcctctaag	1692
DB	1680	GAAGAAGTGAAGAGGCCACCAAAAGTGCCCACTGGTGTACAAAGTGGCGGCCACAAA	1739
QY	1693	tacctgtgtggactagctcagctcagtgctgtgataaagaaggtccctcggaaccatc	1752
DB	1740	GTGCTCATATGGGACTGCTCGGCCCTGGCTGAAGTTCAAGAACATCATCCACTGATC	1799
QY	1753	atgacgatcccttactgagctggccatcacatctgcatacatcaataacocgttttc	1812
DB	1800	GTGATGAGACCGTTCGTGGACCTGGGCATCACCATCTGCATCTGCTGCTCAACACCTCTTC	1859
QY	1813	ttagccgttgagcaccacaacatggatgacaacttaagaccaatactgaaaaataggaac	1872
DB	1860	ATGCCATGGAACATTTACCCCATGACGGAGCACCTTTGACAACGTCCTCACTGTGGGCAAC	1919
QY	1873	tgggttttccagggaaatttccatagcggaaaatgtgtctcaagatcatcgcgctcgacccct	1932
DB	1920	CTGGCTCTCAGAGCATCTTTCACAGCAGAGATGCTTCTGAAGCTGATTTGCCATGAGCCCC	1979
QY	1933	taccactactctcggcgacgctggaatgtttttgacagcagctggtgcccctcctagctc	1992
DB	1980	TACGAGTATTTCCAGCAGGTTGGAATATCTTCGACAGCATCATCTGTCACACCTCAGCTG	2039
QY	1993	gctgagtgtctctacacacactgtctgtataacaaatagggtcttcttcttggcttccctcaga	2052

ILIQMDPLVPGDKIHCLDILFPAFTKNVLGSEGLDSLKNMEEKPMATNLSKASVEP
IATTLRWKQEDSATVYQKAYSRMYLHRSLLTNTLHVPRAEEDGVSLOPEGVYTFMA
NSGIPQKSETASATFPQPSYSDVSYTRGLSDRANINPSSMQONEDEVAKEGNSPGQ"
1487 a 1823 c 1622 g 1412 t
BASE COUNT
ORIGIN

BASE COUNT	1487 a	1823 c	1622 g	1412 t
ORIGIN				

100

Query Match 23.9%; Score 1411.4; DB 10; Length 6344;
Best Local Similarity 57.6%; Pred. No. 0;
Matches 3248; Conservative 0; Mismatches 1921; Indels 474; Gaps 21;

Qy	45	gaagatggagagagggtactaccggtgtatctctcccggaacagcggaatttcgccccctt	104
Db	10	GAAGAATGAGAAAGATGGAGCTCCCTTTGGCTCGGTGGAACTACCAATTTTCAGACGGTT	69
Qy	105	cactccgactctcgctgcataaagaagcgatgctatccaa-----aa	152
Db	70	CATCTCCAGATCACTGGCAGAGATCGAGACGATGTCTGCTCACCGCGAGCCAGAA	129
Qy	153	ggagagaagaagtcctcaagaagcgcgagctgagccccagctcgccctcagcttga	212
Db	130	GGCCAGAACCAACACAGAGGACAGGAGCAAGGGCGAGAACCCAGGCCCTCAGCTGGA	189
Qy	213	cctaagagcctccaggaagttacctaagcttattggtgacattccccctgagctgttac	272
Db	190	CTTGAAGAGCTGTAAACAGCTGCCAAAGTTATGTGGTGAAGTCCAGCAGAACTGGTCGG	249
Qy	273	gaacctctgagagacctggacctactcaagaagaccataagaacattcatggtgtgaa	332
Db	250	GGAGCCCTGGAGAACCTAGACCCCTTCTACAGCACACACCGGACATTCATGTGTGGA	309
Qy	333	caagaaagaacaattatcgcttcacggccaaagcgccctgttctatctcgtggccctt	392
Db	310	TAAAGCAGGACCATTTCCAGATTCAGTGCCACTTGGGCCCTGTGGCTCTTCAGTCCCTT	369
Qy	393	taatccctcagaagcttaagtattgttatctctgtccattcaagctctttagacttcat	452
Db	370	CAACCTGATCAGAAAGACAGCCATCAAAAGTGTCTGTCCATTTCCTGGTGTCTCCATATTCAT	429
Qy	453	catctgcacggtgatcatcaactgtatgttcattgacggcaattctatggagagaagttcga	512
Db	430	CACCATCACTATTTTGGTCACTCGGTGTGATGACCC-----GAACGTGATCT	477
Qy	513	caagacattccogaatactcttoatttgggatttatatttagaagctgtgattaaaa	572
Db	478	TCCAGAGAAATCGAGTAGTACGCTTCACCTGTCAATTACACCTTCGAGGCTCTGATTAAAT	537
Qy	573	attgcgaagccttcatttggatgaatttcctctccgaatccgtgagaactgct	632
Db	538	ACTGCGAAGAGGGTTTGTCTAAATGAGTTCACTTATCTTCAGATCCGTGGAACTGGCT	597
Qy	633	ggactcatctcattggaaacgagatcgcaactgttttcccggaagccaaagtcact	692
Db	598	GGACTTCAGTTCATTACCTTTGGCGTATGTGGGTGCAGCGATAGACCTCCGAGGAA---T	654
Qy	693	ttcagctcttgtaacctccagtggttcaagagctctgaagcgatctcagttatctcagg	752
Db	655	CTCAGGCGTCGGACATTCGAGTCTCAGAGCCCTGAAACTGTTCTGTGATGCCACAG	714
Qy	753	tctgaagctcatctgagtgcccttgcctgcgtcgtgtgaagaagctggttagacgtgatgt	812
Db	715	ACTGAAGTTCATCGTGGAGCCCTGATCCACTCAGTGAGGAAGCTGGCCGACGTGACTAT	774
Qy	813	cctaactctctcctcagcatcttttgcctcgttggtcagcagctgtttcatcaggaa	872
Db	775	CCTCACAGCTCTTCGCTGAGCGCTTTCGCTTGTGGCCCTGCGAGCTCTTTAAAGGGAA	834
Qy	873	tctgaacagagtgattaaagcaactgtggcccaaccctcatccaac-----	924
Db	835	CCTTAAGAACAAATGATCAGAAACGGNACAGATATCCCCACAAAGCTGACAACTCTCATC	894
Qy	925	-----aagatctgtttgaaaggaagaaagatagcgaagacttcaatctgttggtac	977

LPRLMTQDWENLFLQTLRAAGKTYMIFPVVIFIGSFVYLINLIILAVMAYAEQNEA
TLAEQDEKEEFQMLEKFKHOEELEKAKAAQALEGGEADGDTPHSDKDCNGSLDTS
GKGPPRPSCSAESAIISAMEELEAHQKPPWQKCAKHLVIMWCADPWAFKHLIL
LIVMDPFDLGTICIVLNTLFWAMEHYPMTEBFDNVLVSGLVFTGPTAKBWPVLKI
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FASLSLAEDGEMNNQIAIGRIKQWIAFAFTFLGLLHGKILLSKDIMLSLGE
GAGENGESDEKPEPPEDKELKONHILNHVGLTDPGRSSSEMIDHNPILNPPYL
THYVLIASDESLEMPETEOTKELKPLQPLDYDGNSSVSTADYKPEDEPE
EQANPEGELPEECFTEACVKRCPCLVYDIISQGRKMWMTLRRACFKIVEINWETFE
IVPMILLSSGALFEDILYEQRVIRITILEYADKVFTYIFILEMLLWYAGFKYVFT
NACWMLDFLIVDSIISLVANWLGSELGPIKSLRTRALRPLRLLRSRGRVYVNA
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SMYTGCOVMNVKMYNDVNGVYLSLQVATFKGMDIMYAAVDSREKEEPEYEVN
LYMYLYFVFIIFGSPFTNLNFIIVDFNNOQKFKFGKIDIFMTEOKKYFNAWKLL
GSKKPKPIRPNQIQGMVYDFTVKQVFDISIMILICLNMVMTMAVETDDOSOLKVDI
LYNINMVIIVTGCVLKMFALRHYFTIIGNNIFDFVYVILSVGLALSLLIQYFV
STPLRVIRIARIGRVLRIKAGRTULFALMMSLPALFNIGLILLFLVMFYISIFG
MNSFAYKKSIGIDMFNETFNSILICEITTSAGWDGLNPLNLSPPDCDPTLE
NPGTNIKGDGNPSIGICFCFSYIIISFLIVVMYIAIILENFVATERSSBPLACEDD
FMFVETWEKFPDPAQFTDYSLRSDVFTLOEPLKIAKPNKIKLITLDPVPGDKI
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KTQRAYRHLLORSKQASMYRHSQBGNGDCAPEKEGLLANTMKNMYSERKEDNGVQ
SOGREKOSTEDAGPTTEVTAPESSDTALTTPPPSPPPSPQGGTVRPGVKSLV*

BASE COUNT 1347 a 1680 c 1534 g 1326 t
ORIGIN

Query Match 23.8%; Score 1406.4; DB 10; Length 5887;
Best Local Similarity 57.1%; Pred. No. 0;
Matches 2998; Conservative 0; Mismatches 2121; Indels 129; Gaps 19;

QY	66	cccggtgatcttcccgagcagcggaatttccgcccctcacttcgactctctggtcgc	125
DB	22	CACCTTGTCCTCCCTGGTCCCTACCTGCTCGCCCTTCCACCCAGAGTCCCTGGCAGC	81
QY	126	cataaagaagcgg---attgctatccaaaggagagaagaagtcctcaagaacagcgc	182
DB	82	CATAGAACACGGGCAATGAGGAGGAAGCCGGCTGCACGGAACAAGCAATGGAGAT	141
QY	183	agctgagccccagcctcgctcagcttgacctaaaggcctcaggaagttaactaagct	242
DB	142	TGAAGAGCCTTGAGCGGAGCAGCGACGTGACCTGGAAGCTGGCAAGACCTCCACTCAT	201
QY	243	ttatggtgacattccccctgagctgttacgaaacctctgagagacctgagccctacta	302
DB	202	CTATGGGACCCCTCCACTGAAGTCATTGGCGTCCCTCGAGGACCTGGACCCCTACTA	261
QY	303	caagaccataagacattcatgtgttgaaacaagaagaacaatttatcgcttcagcgc	362
DB	262	CAGTGACAAGAACCTTCATTGTGCTCAACAAGGAAGGCCATCTTCCGATCTCTGC	321
QY	363	caagcgggctgttgaattctcgggcttttaattccccctcagaagcttaattgattat	422
DB	322	CACCCCTGCCCTCTACATGTGAGCCCTTCAGCATCGTCCGGCGGTGCTATCAAGGT	381
QY	423	ctctgtccattcagcttttagcattgtccatctgacgctgacggtgacatcaactatgtt	482
DB	382	GCTCATCCAGCGGTGTTCAGCATGTTTCATCATGATCACCATTCTTGACCAACTGCGGT	441
QY	483	catggcgaattctatgagagaagtttcgacacgacattcccgaaatcgtcttctatgg	542
DB	442	CATGACCATGACNAACCGCTCTTGTGGTCCAAGGAGCT---GGAGTACACCTTCACAG	498
QY	543	gatttatatttagaagctgattataatttgcaagaggtcttcaattgtgattgagtt	602
DB	499	GATCTACACCTTTGAGTCCCTCATTAAGATGCTGGCCCGAGGCTTTTGCAATTGACTT	558
QY	603	tcccttctccgagatccgtggaactgctggacttcaattgtcatgtggaacagcgcgc	662
DB	559	CACATTCTCCGAGACCCCTGGAACCTGGCTGGACTTTCAGTGTCTATCATCAATGGCGTACGT	618
QY	663	aactbtgtttcccgaggcagccaagtcatttccagctctctgactcctccagctggtcag	722
DB	619	GACAGAGTTTGTGG---ACTTGGGCAACATCTCAGCCCTGAGGACCTTCGCTGTGTCGG	675
QY	723	agcttgaagcgatatttcagttatcagttatcaggtctgaaggtcactgtaggtgacctgctg	782
DB	676	GGCCCTGAAAAACCATCAGGTCATCCAGGGCTGGAAGACCATCTGAGGAGCCCTGATCCA	735
QY	783	ctcggtgaagaagctgtagacgtgtagctcactctcttctgctcactcagctcttgc	842
DB	736	GTCTGTGAAAAACCTCTCGGATGATGATCCTCACTGTCTTCTGCTGAGCGCTTTGC	795
QY	843	ccctggttcagcagctgcttcattggaattctgtaaccagaagtgtat---taagacaaa	899
DB	796	CCTGGTGGGCTCGAGCTTTTTCATGGGAAACCTCGCTCAGAACTGCGTGGCTGGCCCC	855
QY	900	ctgtggcccccaacctgcattcccaagaagattcttggaaaaagaaagataagcaaga	959
DB	856	GCCCATGAAATGACCAACACACCTGGTGTGTAATGATACGTGGTACGGCAATGACAC	915
QY	960	cttcaataatgtgtggtacctgctcgccagcagaccctgtcccgaatgttctactgctga	1019
DB	916	CTGCTACGGCAATGACACCTGGTGTGCAATGACACTTGGCAACAGCCAGGAGCTGGGT	975
QY	1020	taaaaccac-----attgaaccagacaataattatacaaaagtttgacaactt	1067
DB	976	CAGCAACTCTACCTTTGACTGGGAGGCTACATCAATGACGAAGGAACTTCTATTCTT	1035
QY	1068	tgctggtctctctgcgatgttccgggttatgaactcaagaactcctggagaggtttaa	1127
DB	1036	GGAGGCTTCCAAATGATGCCCTGCTCTGTGGGAATAGCAGTATGCGGGGACTGCCCTGA	1095
QY	1128	ccgacagatcctcgagacctctgggtactcttcttcttcttcttcttcttcttctt	1187
DB	1096	GGCTACGAATGATGAAGCTGGGAGGAACCCCAACTATATGGCTACACAGCTACGACAC	1155
QY	1188	cctgggtcctcttactcgttaacctaacctggctgtgttgcacctggtcttatgaaga	1247
DB	1156	CTTCAGCTGGGCTTCTGCTCTCTTCCGCTCTCATGACGACGACTACTGGGAGAACCT	1215
QY	1248	acagaacagaaaatgtagctctgagacagagggccaagagagaagaatgtttcaggaagccc	1307
DB	1216	TTTCCAGCTACCCCTTCGAGCTCTGGCAAGACCTACATGATCTTCTTGTGTGTCATCAT	1275
QY	1308	gcagctgttaaggaggagaagagcctggttgcctatgggaattgacagaagttccct	1367
DB	1276	CTTCTGGGTTCCTTCTACCTCATCAATCTGATCCTGGCGGTGCTGGCCATGGCATATGC	1335
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QY	1668	atgtgggaataattgctccttaagtacctggtgtgggaactgtacctgagtgctgtg	1727
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QY	1728	cataaagaaggttcctgcgcgaccatcatgacggtatcccttctactgagctggccatcaccat	1787

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RESULT 15

RNY17153

LOCUS	RN17153	5523 bp	ROD	25-AUG-1998
DEFINITION	Rattus norvegicus mRNA for skeletal muscle type 1 voltage-gated sodium channel.			

ACCESSION Y17153

VERSION Y17153

KEYWORDS

RECEIVED
JAN 10 1988

SOURCE	ORGANISM	NOTWAY	Rattus
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PROKARYOTIC
EUKARYOTIC

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

REFERENCE

1 (bases 1 to 5023)

REFERENCE

AUTHORS

Diss, J.K., Stewart, D., Fraser, S.P., Black, J.A., Dib-Hajj, S.,
Wayman, S.G., Archer, S.N. and Diamant, M.B.

TITLE Expression of skeletal muscle-type voltage-gated Na⁺ channel in rat waxman, S.G., Achter, S.N. and Djafarzadeh, M.B.

JOURNAL OF THE
FEBRUARY 1991
AND HUMAN

JOURNAL OF MEDICAL PHYSICS 982736

MEDLINE 982736
REFERENCE 2 / 62

REFERENCE
AUTHORS

AUTHORS	TITLE	Abstract	Direct
Archer	Direct		

: TITLE
JOURNAL
Submitted (21-APR-1998) S.N. Archer, International Marine Centre,
Direct Submission

FEAMIDES
Locall

FEATURES

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DB	3092	TCCTTATGATCTGTCTACGACGTGGAGCCCTGGCCCTTCGAAGACATCTACATTTGAACAGC	3151
QY	3230	ggccccaagttagaaaaactaaaggtgaccgataataattttcacaattattttctctcc	3289
DB	3152	GACGAGTCATCCGCACCATCTCTGGAAATAGCCGCACAAAGGTCTTTCACCTACATCTTCATCC	3211
QY	3290	tggaaatgatcctgaagtgggtggcctttggattcccgagggtattttccacagtgccctggt	3349

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 18:35:20 ; Search time 478.33 Seconds
(without alignments)
10569.370 Million cell updates/sec

Title: US-09-646-224A-1
Perfect score: 5897
Sequence: 1 ggaagccatagtgccctga.....gaaagaaaaa 5897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5897	100.0	5897	20	AAZ21480
2	5853.8	99.3	5875	22	AAF30102
3	5822.4	98.7	5908	20	AAZ21480
4	5803.8	98.4	5875	20	AAZ21480
5	5295.6	89.8	5334	20	AAZ21480
6	4633.8	78.6	5822	22	AAF30103
7	4573.8	77.6	5822	20	AAF30101
8	3242.6	55.0	5860	22	AAF30101
9	2162.8	36.7	3701	22	AAF30104
10	2050.8	34.8	3638	20	AAZ21480
11	1411.4	23.9	6344	22	AAF57009

12	1405.2	23.8	6527	18	AAZ21480
13	1399	23.7	6524	18	AAZ21480
14	1384.4	23.5	5874	22	AAF570016
15	1326.8	22.5	7555	16	AAQ81328
16	1325.6	22.5	6048	19	AAV09029
17	1325.6	22.5	6048	22	AAZ21480
18	1311.4	22.2	6048	22	AAZ21480
19	1310.6	22.2	7555	11	AAQ05831
20	1229.6	20.9	7052	18	AAZ21480
21	1168.4	19.8	5977	19	AAV58420
22	1168.4	19.8	6007	19	AAV58421
23	1168.4	19.8	6556	19	AAV58419
24	1168.4	19.8	6586	19	AAV58423
25	1100.8	18.7	6452	17	AAZ30193
26	1096.6	18.6	7053	21	AAZ30193
27	1088.4	18.5	8349	22	AAH55793
28	1088.4	18.5	8349	22	AAH55794
29	1082	18.3	9112	22	AAH55823
30	1082	18.3	9112	22	AAH55824
31	1080.6	18.3	8378	22	AAH55764
32	1079	18.3	8378	22	AAH55763
33	1017.6	17.3	6371	17	AAZ30194
34	1017.6	17.3	6404	17	AAZ30195
35	866.2	14.7	3033	17	AAZ30192
36	763.4	12.9	6519	20	AAV25500
37	676.6	11.5	6513	17	AAZ33238
38	676.6	11.5	6513	17	AAZ18986
39	633	10.7	6318	19	AAV40629
40	633	10.7	6318	20	AAV82498
41	632.2	10.7	2573	18	AAZ77804
42	630.2	10.7	6315	19	AAV40630
43	630.2	10.7	6315	20	AAV82499
44	559	9.5	856	20	AAZ60242
45	373.2	6.3	930	21	AAA53319

ALIGNMENTS

RESULT	1
AAZ21480	
ID	AAZ21480 standard; cDNA; 5897 BP.
XX	
AC	AAZ21480;
XX	
DT	03-DEC-1999 (first entry)
XX	
DE	Rat sensory neurone specific 2a nucleotide sequence.
XX	
KW	Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;
KW	voltage gated; hypersensitivity; ss.
XX	
OS	Rattus sp.
XX	
FT	Key Location/Qualifiers
CDS	49..5346
FT	/*tag= a
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XX	
XX	WC9947670-A1.
PD	23-SEP-1999.
XX	
XX	18-MAR-1999; 99WO-GB00838.
XX	
PR	18-MAR-1998; 98GB-0005793.
XX	
PA	(GLAX) GLAXO GROUP LTD.
XX	
PI	Grose DT, Hick CA, Tate SN;
XX	
XX	WPI; 1999-562112/47.
DR	P-PSDB; AAY41668.

XX Mammalian sodium channel protein for treating pain and hypersensitivity
PT Claim 4; Page 52-58; 73pp; English.
PS The present sequence encodes rat sensory neurone specific 2a (SNS-2a).
XX SNS-2a is a sodium channel protein. SNS-2a can be used in a method for
CC the identification of a modulator of a sodium channel, and for assaying
CC for compounds which modulate sodium flux. The sodium channel modulators
CC can be used in a medicament for the treatment of pain or
CC hypersensitivity.
XX Sequence 5897 BP; 1474 A; 1471 C; 1435 G; 1517 T; 0 Other;
SQ

Query Match 100.0%; Score 5897; DB 20; Length 5897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 gaggccatacgggcccctgacccctctctgtaccaggagaagagatggaggagag 60
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Db 4441 ctccctcttcttgatgatgtctctccctctctctcttcaacatcggtctgtctcttc 4500
QY 4501 ctggtgatgttcaattacgccatttttggatgagtggttttcccaagtgaagaagggc 4560
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QY 4621 cagataacacttcggtggtggatatacctctcaacccctctgctgaggcacaagaa 4680
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QY 5881 aaaaaaaaaaaaaaa 5897
Db 5881 aaaaaaaaaaaaaaa 5897

RESULT 2

AAF30102

ID AAF30102 standard; cdna; 5875 BP.

XX

AC AAF30102;

XX

DT 30-APR-2001 (first entry)

XX

DE Rat sodium channel NaN cdna.

XX

KW Sodium channel; NaN; rat; tetrodotoxin resistant; pain;

KW paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;

RW diagnosis, ss.

XX

OS Rattus norvegicus.

XX

FH Key Location/Qualifiers

FT CDS 41..5338

FT /*tag= a

XX

FN W0200105831-A1.

XX

PD 25-JAN-2001.
 XX
 PF 14-JUL-2000; 2000WO-US19342.
 XX
 PR 16-JUL-1999; 99US-0354147.
 XX
 PA (UYA) UNIV YALE.
 XX
 PI D1b-Hajj S, Waxman SG;
 XX
 PI WPI: 2001-103147/11.
 DR P-PSDB; AAB20122, AAB20123.
 XX
 PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium
 channels, useful for preventing, diagnosing and treating pain,
 PT paraesthesia and/or hyperexcitability phenomena -
 XX
 XX Example 1; Fig 1; 162pp; English.
 XX
 CC The present sequence is that of cDNA encoding a novel rat
 CC tetrodotoxin resistant sodium channel, termed NaN (see AAB20122).
 CC The cDNA was isolated from a dorsal root ganglia tissue cDNA
 CC library by PCR amplification using generic primers (from conserved
 CC regions of a subunit sodium channel proteins) and NaN-specific
 CC primers (see also AAF30105-19), and RACE amplification. The
 CC open reading frame shows 73% similarity to the human NaN sequence
 CC (see AAF30101). NaN belongs to the a-subunit voltage-gated sodium
 CC channel protein family and produces a TTX-R sodium current. Such
 CC channels underlie the generation and propagation of impulses in
 CC excitable cells such as neurons and muscle fibres. Preferential
 CC expression of NaN on sensory neurons innervating the body (dorsal
 CC root ganglia) and the face (trigeminal ganglia), but not on other
 CC neurons, makes it a very useful target for diagnostic and/or
 CC therapeutic uses in relation to acute and/or chronic pain
 CC pathologies. A claimed method of treating pain, paraesthesia
 CC and/or hyperexcitability phenomena in a human or animal subject
 CC involves administering an agent that alters sodium current flow
 CC through NaN channels, or which modulates transcription or
 CC translation of NaN mRNA, in dorsal root ganglia or trigeminal
 CC neurons. NaN nucleic acids are used in gene therapy to correct
 CC disorders associated with decreased sodium channel expression or
 CC (antisense) to down-regulate NaN expression, in the diagnosis of
 CC disease, and in the recombinant production of NaN polypeptides.
 XX
 XX Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 2 other;

Query Match 99.3%; Score 5853.8; DB 22; Length 5875;
 Best Local Similarity 99.8%; Pred. NO. 0;
 Matches 5861; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 9 acggtgccctgacctctgtaccaggagacacaggggtgaagatggaggaggtactacc 68
 DB 1 acggtgccctgacctctgtaccaggagacacaggggtgaagatggaggaggtactacc 60
 QY 69 ggtgatctcccgacgagcggaattccgcgcccttcactccgactctctggtgccat 128
 DB 61 ggtgatctcccgacgagcggaattccgcgcccttcactccgactctctggtgccat 120
 QY 129 aaagaagcggattgctatccaaagagagaggaagagaggtccaaagacaaagcgagctga 188
 DB 121 agagaagcggattgctatccaaagagagaggaagagaggtccaaagacaaagcgagctga 180
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 QY 249 tgacattccccctgagcttggttacgaaacctctggaggacctgagaccttactacaaga 308
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 QY 309 coataagacattcatggtttgaacaaagaaagacaatttatcgcttcagcgcccaagcg 368
 DB

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 DB 361 ggcctgttcattctgtgggccccttttaattccctcagaagcttaattgattctctctgt 420
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QY 2139 aaacctgactgtggttcctgactatcgttggttctcaatttttctggtgggcatcggt 2198
DB 2169 aaacctgactgtggttcctgactatcgttggttctcaatttttctggtgggcatcggt 2228
QY 2199 ctccggcacaagtttaacaagaccctcctacgcaccacacagagcgcccaagcgcgctg 2258
DB 2229 ctccggcacaagtttaacaagaccctcctacgcaccacacagagcgcccaagcgcgctg 2288
QY 2259 gcacatggaataattctacacactcctctcgttggtgttcctcgcatctctgtgggaatg 2318
DB 2289 gcacatggaataattctacacactcctctcgttggtgttcctcgcatctctgtgggaatg 2348
QY 2319 gatcgagaacatgtgggctgcatgaggaataggaagcgctcccggttggcatcattgt 2378
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QY 2439 gctcaattctctcagcaatgagaggaatgaggcctggaaggagagaccaggaaaac 2498
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DB 2589 tcagagtttttctgcaagaaatgcaggaggaagaaactcccaagccaaagagacaac 2648
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QY 3279 tatttctcctcgaaatgatcctgaagtgggtggcctttggattccggaggtatttccac 3338
DB 3309 tatttctcctcgaaatgatcctgaagtgggtggcctttggattccggaggtatttccac 3368
QY 3339 cagtgcctggtgcctggcttgcatttccctcatttgttggtgtctgtctgctcagatctca 3398
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DB 3429 tctacaaagtgtgaagttcctccggactctgcgggcccctgagacctctgcggcgctgtc 3488
QY 3459 ccagtttgaggaatgaagttgtctcagccctgatcagcgccatacctgcattct 3518
DB 3489 ccagtttgaggaatgaagttgtctcagccctgatcagcgccatacctgcattct 3548
QY 3519 caatgtctgtgctgcctcattttctgctgcttatttgttatcttggaggataaattt 3578

QY 5739 ctacgggtgtctctaccagcatcacagaattgggtgtatgactcaaacctaaagcatga 5798
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 QY 5799 ctctgactgtcagtcagcaccgccgactttcagacgtcccaatctctgtcccaggtgtct 5858
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 Db 5829 ctctgactgtcagtcagcaccgccgactttcagacgtcccaatctctgtcccaggtgtct 5888
 |||||
 QY 5859 aacgaataaataagtaaaag 5878
 |||||
 Db 5889 aacgaataaataagtaaaag 5908
 |||||

RESULT 4

AAX87600

ID AAX87600 standard; cDNA; 5875 BP.

XX

AC AAX87600;

XX

DT 26-OCT-1999 (first entry)

XX

DE Rat sodium channel NaN cDNA.

XX

KW NaN; sodium channel; ion transport; rat; dorsal root ganglia;

KW pain; paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 41..5338

FT /*tag= a

FT misc_feature 5551..5600

FT /*tag= b

FT /note= "these bases represent nucleotides missing

FT from the sequence given in Fig 1 of the

FT specification. The nucleotides are

FT included to maintain the nucleotide

FT numbering given in the specification for

FT this DNA sequence"

XX

PN W09938889-A2.

XX

PD 05-AUG-1999.

XX

PE 29-JAN-1999; 99WO-US02008.

XX

PR 20-NOV-1998; 98US-0109402.

PR

PR 29-JAN-1998; 98US-0072990.

XX

XX (UYVA) UNIV YALE.

XX

XX D1b-Hajj S, Waxman S;

PI

XX WPI; 1999-479168/40.

XX

DR P-PSDB; AAY06596.

DR

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CC that express NaN, methods for identifying agents that modulate NaN
 CC channel activity or NaN channel mRNA transcription or translation,
 CC and a method for using such agents to treat acute or chronic pain,
 CC paraesthesia and hyperexcitability phenomena. The preferential
 CC expression of NaN in sensory DRG and trigeminal neurons provides a
 CC target for selectively modifying the behaviour of these nerve cells
 CC while not affecting other nerve cells in the brain and spinal cord.
 CC The NaN gene has been named Scn1a.

XX
 SQ Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 52 other;

Query Match

Best Local Similarity 98.4%; Score 5803.8; DB 20; Length 5875;

Mismatches 5811; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 9 acggtgccctgacatctctgtaccaggaagacaggggtgaagatggagagaggtactacc 68
 |||||

Db 1 acggtgccctgacatctctgtaccaggaagacaggggtgaagatggagagaggtactacc 60
 |||||

QY 69 ggtgatctcccgacagcgggaatttcgcccccttcacctccgactctctgctgccat 128
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Db 61 ggtgatctcccgacagcgggaatttcgcccccttcacctccgactctctgctgccat 120
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QY 129 aaagaagcggatgtctatccaaaaggagagaaagaaagtcacaaagacagcgccagctga 188
 |||||

Db 121 agagaagcggatgtctatccaaaaggagagaaagaaagtcacaaagacagcgccagctga 180
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QY 189 gccccagcctcggcctcagcttgacctaaggcctccaggaagtacctaaagctttatgg 248
 |||||

Db 181 gccccagcctcggcctcagcttgacctaaggcctccaggaagtacctaaagctttatgg 240
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QY 249 tgacattccccctgagctgtttacgaaacctctggagacctggacccctactacaaga 308
 |||||

Db 241 tgacattccccctgagctgtttacgaaacctctggagacctggacccctactacaaga 300
 |||||

QY 309 ccataagacattcatgtgttgaaacaaagaaacaaatattatcgctcagcgcccaagcg 368
 |||||

Db 301 ccataagacattcatgtgttgaaacaaagaaacaaatattatcgctcagcgcccaagcg 360
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QY 369 ggccttgcttattctggggccttttaacccctcagaagcttaatgatctgctatctgt 428
 |||||

Db 361 ggccttgcttattctggggccttttaacccctcagaagcttaatgatctgctatctgt 420
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QY 429 ccattcagctcttagcatgttcatctgcacggtgatcatcaactgtatgtttcagtc 488
 |||||

Db 421 ccattcagctcttagcatgttcatctgcacggtgatcatcaactgtatgtttcagtc 480
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QY 489 gaattctatggagagaagtttcgacaacgacattcccgaatacgtcttcattgggatta 548
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Db 481 gaattctatggagagaagtttcgacaacgacattcccgaatacgtcttcattgggatta 540
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QY 549 tattttagaagctgtgattataatttggaagaggtcttcattgtggatgagtttctct 608
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Db 541 tattttagaagctgtgattataatttggaagaggtcttcattgtggatgagtttctct 600
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QY 609 cctccagatccctggaactggtgacttcattgttcattggaacagcgtacacacttg 668
 |||||

Db 601 cctccagatccctggaactggtgacttcattgttcattggaacagcgtacacacttg 660
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QY 669 ttttcggggcagccaaagctcaattttcagctcttcgttaccttcgagtggttcagagctct 728
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Db 661 ttttcggggcagccaaagctcaattttcagctcttcgttaccttcgagtggttcagagctct 720
 |||||

QY 729 gaaggcgatttcaggttatctcaggtctgaaggttcagtaggtgcctctgctgcgtcgtt 788
 |||||

Db 721 gaaggcgatttcaggttatctcaggtctgaaggttcagtaggtgcctctgctgcgtcgtt 780
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QY 789 gaagaagctgtgacagctgagtcctcactctctctgctcagcatctttgccctcgtt; 848
 |||||

Db 781 gaagaagctgtgacagctgagtcctcactctctctgctcagcatctttgccctcgtt; 840
 |||||

QY 849 cgggtcagcagctgttcagtggaagaaattctgaaccagagaagtgtattaaagcacactgtgccc; 908
 |||||

CC This is the nucleotide sequence of an isolated nucleic acid which
 CC encodes the rat NaN channel (see AAY06596), a previously unidentified
 CC voltage gated sodium channel protein that is preferentially
 CC expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and
 CC which produces a TTX-R sodium current. The NaN channel cDNA was
 CC obtained from Sprague-Dawley rat DRG cDNA by PCR and RACE
 CC amplification (see also AAX87603-17). Rat, mouse and human NaN
 CC nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are
 CC provided. The invention also includes expression vectors and
 CC transformed host cells, methods for identifying tissues and cells

Db 841 cggcagcagctgttcattggaattctgaaccagaagtgatttaagcaacaactgtggccc 900
Qy caaccctgcattcaacaagattgcttgaagaagaaagatagcgaagacttcaaat 968
Db caaccctgcattcaacaagattgcttgaagaagaaagatagcgaagacttcaaat 960
Qy gtgtggtacctggctcggcagcagaccctgtcccaatggtcttacgtgcgaataaaccac 1028
Db gtgtggtacctggctcggcagcagaccctgtcccaatggtcttacgtgcgaataaaccac 1020
Qy attgaaccagacaataatatacaaaagttagacaactttggctgtgctcttcttcgccat 1088
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Qy gttccgggttatgactcaagactcctcggagagagctttaccgacagatcctcggaccctc 1148
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Qy	4569	cgacgacatctca	acttcgaagc	ctttacgggc	agcatgct	gtctctccagata	aac	4628
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Db	5101	ggaggagaagtt	tatggaggcca	accctttta	gaagctct	ctacgag	cccatagtcacac	5160
Qy	5169	caccagagaga	ggaggagac	aaggccgc	ctcatcca	gagggctacc	gaggaacat	5228
Db	5161	caccagagaga	ggaggagac	aaggccgc	ctcatcca	gagggctacc	gaggaacat	5220
Qy	5229	catgacgaat	atgctcaaac	ctgggctga	gagacag	gtcaagt	ctcatccac	5288

Db 734 ggtcactgtagtgccctgctgcctcggtagaagaagctggtagacgtgtagtctccac 793
Qy 819 tctcttctgctcagcatcttgccttgcctggtcagcagctgttcaatggaaattctgaa 878
Db 794 tctcttctgctcagcatcttgccttgcctggtcagcagctgttcaatggaaattctgaa 853
Qy 879 ccagaagtgtattaaagacacactgtggcccaacccctgcacccaagaagattgcttga 938
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Qy 939 aaaggaagaaatagcgaagaactcataatgtgtgtacctggtcctgcgcagacacctg 998
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 Db 5294 gccaaggtcaaggttcacaaatgactgaaccctcatct 5331

RESULT 6

AAF30103

ID AAF30103 standard; cDNA: 5822 BP.

XX AC AAF30103;

XX 30-APR-2001 (first entry)

DT Mouse sodium channel NaN cDNA.

DE Sodium channel; NaN; Scn1a; mouse; tetrodotoxin resistant; pain;

KW paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;

KW diagnosis; ss.

XX Mus musculus.

XX Key

FH CDS Location/Qualifiers

FT 19..5316

FT /*tag= a

FT polyA_signal 5789..5794

FT /*tag= b

FT polyA_site 5800..5822

FT /*tag= c

XX WO200105831-A1.

XX 25-JAN-2001.

XX 14-JUL-2000; 2000WO-US19342.

XX 16-JUL-1999; 99US-0354147.

XX (UYVA) UNIV YALE.

XX D1b-Hajj S, Waxman SG;

XX WPI: 2001-103147/11.

XX P-PSDB; AAB20124.

XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium

XX channels, useful for preventing, diagnosing and treating pain,

XX paraesthesia and/or hyperexcitability phenomena .

XX Example 3; Fig 7A; 162pp; English.

XX The present sequence is that of cDNA encoding a novel mouse

XX tetrodotoxin resistant sodium channel, termed NaN (see AAB20124).

XX The cDNA was isolated from trigeminal ganglia cDNA using primers

XX (see AAF30102-21) based on rat NaN sequences. Mouse NaN shows

XX 68% similarity to human NaN (see AAB20121). The gene encoding NaN,

XX termed Scn1a, is located on mouse chromosome 9. NaN belongs to the

XX a-subunit voltage-gated sodium channel protein family and produces

XX a TTX-R sodium current. Such channels underlie the generation and

XX propagation of impulses in excitable cells such as neurons and

XX muscle fibres. Preferential expression of NaN on sensory neurons

XX innervating the body (dorsal root ganglia) and the face (trigeminal

XX ganglia), but not on other neurons, makes it a very useful target

CC for diagnostic and/or therapeutic uses in relation to acute and/or
 CC chronic pain pathologies. A claimed method of treating pain,
 CC paraesthesia and/or hyperexcitability phenomena in a human or animal
 CC subject involves administering an agent that alters sodium current
 CC flow through NaN channels, or which modulates transcription or
 CC translation of NaN mRNA, in dorsal root ganglia or trigeminal
 CC neurons. NaN nucleic acids are used in gene therapy to correct
 CC disorders associated with decreased sodium channel expression or
 CC (antisense) to down-regulate NaN expression, in the diagnosis of
 CC disease, and in the recombinant production of NaN polypeptides.
 XX
 XX Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 1 other;

Query Match

Best Local Similarity 78.6%; Score 4633.8; DB 22; Length 5822;

Matches 5193; Conservative 0; Mismatches 603; Indels 78; Gaps 12;

QY 40 aggtgaagatggagagaggtactaccgggtgatttcccgagcagagcggaatttcgcg 99

Db 10 aggtgaagatggagagaggtactaccgggtgatttcccgagcagagcggaatttcgcg 69

QY 100 ccttcacattccgactctctgctgccataaagaagcgattctccaaaaaggagag 159

Db 70 ccttcacattccgactctctgctgccataaagaagcgattctccaaaaaggagag 129

QY 160 aagaatccaaagacagcgcgcagctgagcccgcccgctcgctcagcttgacctaaag 219

Db 130 aagaatccaaagacagcgcgcagctgagcccgcccgctcgctcagcttgacctaaag 189

QY 220 gctccaggaagttaaccttaagctttatggtgacattccccctcgagcttgtagaacct 279

Db 190 gctccaggaagttaaccttaagctttatggtgacattccccctcgagcttgtagaacct 249

QY 280 ctggaggaacctggaccctactacaaagaccataaagacattcattggttgacaagaaga 339

Db 250 ctggaggaacctggaccctactacaaagaccataaagacattcattggttgacaagaaga 309

QY 340 agacaatttatcgcttcagcgcgaagcggccttgctcattctggggccttttaacc 399

Db 310 agacaatttatcgcttcagcgcgaagcggccttgctcattctggggccttttaacc 369

QY 400 ctgagaagcttaagtattgattgattctctgtccattcttcagttcttttagcttcattctgc 459

Db 370 atcagaagcttcattgattgattctctgtccattcttcagttcttttagcttcattctgc 429

QY 460 acggtgatcatcaactgattgattcttcattgaggaa-----ttctatggagagaatttcgcac 513

Db 430 acggtgatcatcaactgattgattcttcattgaggaa-----ttctatggagagaatttcgcac 489

QY 514 aacgacattcccgaaatacgtcttcattgggatttatatttagaagctgtgataaata 573

Db 490 agtaacattcccgaaatacgtcttcattgggatttatatttagaagctgtgataaata 549

QY 574 ttggcagaaggttctcattggtgagattttctctctcccgagatccgtgggaactggctg 633

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DB 1030 acaaaacttgacagctttggctggtcctttctcgccatgttccgggttatgactcaagac 1089
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RESULT 7

AXH87601
 ID AAX87601 standard; cDNA; 5822 BP.

AC AAX87601;

XX 26-OCT-1999 (first entry)

XX Mouse sodium channel NaN cDNA.

XX NaN; sodium channel; ion transport; mouse; dorsal root ganglia;
 KW pain; paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT 19..5316

FT CDS /tag= a

FT misc_feature 4201..4260

FT /tag= b

FT /note= "these bases represent nucleotides missing
 from the sequence given in Fig 7 of the
 specification. The nucleotides are
 included to maintain the nucleotide
 numbering given in the specification for
 this DNA sequence"

FT polyA_signal 5789..5794

/*tag= c

WO938889-A2.

05-AUG-1999.

29-JAN-1999; 99WO-US02008.

20-NOV-1998; 98US-0109402.

29-JAN-1998; 98US-0072990.

(UYXA) UNIV YALE.

Dib-Hajj S, Waxman S;

WPI; 1999-479168/40.

P-PSDB; AAY06597.

New isolated nucleic acids encoding sodium channels, used to develop
 products for treating acute or chronic pain or hyperexcitability
 phenomena

Claim 1; Fig 7A1-3; 91pp; English.

This is the nucleotide sequence of an isolated nucleic acid which
 encodes the mouse NaN channel (see AAY06597), a previously unidentified
 voltage gated sodium channel protein that is preferentially
 expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and
 which produces a TTX-R sodium current. The NaN channel cDNA was
 obtained from mouse trigeminal ganglia cDNA by PCR amplification
 using rat NaN-based primers (see AAX87618-19). Rat, mouse and human
 NaN nucleic acids (see RAX87600-02) and polypeptides (see AAY06596-98)
 are provided. The invention also includes expression vectors and
 transformed host cells, methods for identifying tissues and cells
 that express NaN, methods for identifying agents that modulate NaN
 channel activity or NaN channel mRNA transcription or translation,
 and a method for using such agents to treat acute or chronic pain,
 paraesthesia and hyperexcitability phenomena. The preferential
 expression of NaN in sensory DRG and trigeminal neurons provides a
 target for selectively modifying the behaviour of these nerve cells
 while not affecting other nerve cells in the brain and spinal cord.
 The gene encoding NaN has been named Scn1a.

Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 61 other;

Query Match

Best Local Similarity 77.6%; Score 4573.8; DB 20; Length 5822;

Matches 5133; Conservative 0; Mismatches 663; Indels 78; Gaps 12;

QY 40 aggggtgaagatggagagaggttactaccggtgtatcttcccgagacagaggaatttcgcg 99

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QY 100 cccttcacttcgactctctgctgcataaagaagcgaattgtctacaaaggagag 159

DB 70 cccttcacttcgactctctgctgcataaagaagcgaattgtctacaaaggagag 129

QY 160 aagaagtcacaaagacagcggcgagctgagcccgctcgctcagcttgacctaaag 219

DB 130 aagaagtcacaaagacagcggcgagctgagcccgctcgctcagcttgacctaaag 189

QY 220 gcttcaggaaagttacctaagctttatggtgacattccccctcagcttgtttagaaccct 279

DB 190 gcttcaggaaagttacctaagctttatggtgacattccccctcagcttgtttagaaccct 249

QY 280 ctggaggacctgacccctactactaagaacacataaagcattcattgttgaacagaaa 339

DB 250 ctggaggacctgacccctactactaagaacacataaagcattcattgttgaacagaaa 309

QY 340 agaacaattatcgcttcagcgcgaagcggcctgttcaattctgggcttttaacc 399

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DB		
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AAAF30101		
ID	AAF30101 standard; cDNA; 5860 BP.	
XX	AC	AAAF30101;
XX	AC	
XX	DT	30-APR-2001 (first entry)
XX	XX	
DE	DE	Human sodium channel NaN cDNA.
XX	XX	
KW	KW	Sodium channel; NaN; human; tetrodotoxin resistant; pain;
KW	KW	paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
KW	KW	diagnosis; ss.
XX	XX	
OS	OS	Homo sapiens.
XX	XX	
EH	EH	Key Location/Qualifiers
FT	FT	CDS 31..5402
FT	FT	/tag= a
XX	XX	
DN	DN	WO200105831-A1.
XX	XX	
PD	PD	25-JAN-2001.
XX	XX	
RF	RF	14-JUL-2000; 2000WO-US19342.
XX	XX	
PR	PR	16-JUL-1999; 99US-0354147.
XX	XX	(UYYA) UNIV YALE.
PA	PA	Dib-Hajj S, Waxman SG;
PI	PI	WPI; 2001-103147/11.
DR	DR	P-PSDB; AAB20121.
DR	DR	
XX	XX	
PT	PT	Nucleic acid molecules encoding human tetrodotoxin resistant sod
PT	PT	channels, useful for preventing, diagnosing and treating pain,
PT	PT	paraesthesia and/or hyperexcitability phenomena -
XX	XX	
FS	FS	Claim 1; Fig 1IA; 162pp; English.
XX	XX	
CC	CC	The present sequence is that of cDNA encoding a novel human
CC	CC	tetrodotoxin resistant sodium channel, termed NaN (see AAB20121).
CC	CC	The cDNA was isolated from a human dorsal root ganglia tissue CD
CC	CC	library by PCR amplification (see also AAF30122-23). NaN belong
CC	CC	to the a-subunit voltage-gated sodium channel protein family and
CC	CC	produces a TTX-R sodium current. Such channels underlie the
CC	CC	generation and propagation of impulses in excitable cells such
CC	CC	neurons and muscle fibres. Preferential expression of NaN on
CC	CC	sensory neurons innervating the body (dorsal root ganglia) and
CC	CC	face (trigeminal ganglia), but not on other neurons, makes it a
CC	CC	very useful target for diagnostic and/or therapeutic uses in
CC	CC	relation to acute and/or chronic pain pathologies. A claimed
CC	CC	method of treating pain, paraesthesia and/or hyperexcitability
CC	CC	phenomena in a human or animal subject involves administering an
CC	CC	agent that alters sodium current flow through NaN channels, or
CC	CC	which modulates transcription or translation of NaN mRNA, in
CC	CC	dorsal root ganglia or trigeminal neurons. NaN nucleic acids
CC	CC	are used in gene therapy to correct disorders associated with
CC	CC	decreased sodium channel expression or (antisense) to down-regul
CC	CC	NaN expression, in the diagnosis of disease, and in the recombin
CC	CC	production of NaN polypeptides.
XX	XX	
SO	SO	Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 other:

Query Match 55.0%; Score 3242.6; DB 22; Length 5860;
Best Local Similarity 76.2%; Pred. No. 0;

Matches 4174; Conservative 0; Mismatches 1199; Indels 102; Gaps 11;

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Qy 2688 -----agacatggcttctgtacactggagggcggtgtgtgtgtgtgtgtgtgtgtgtgtgt 2736

CC for a portion (see AAY06596) of human Nan, a previously unidentified
 CC voltage gated sodium channel protein that is preferentially
 CC expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and
 CC which produces a TTX-R sodium current. The Nan channel cDNA was
 CC obtained from human DRG tissue cDNA by PCR amplification (see also
 CC AAX87620-22). Rat, mouse and human Nan nucleic acids (see AAX87600-02)
 CC and polypeptides (see AAY06596-98) are provided. The invention also
 CC includes expression vectors and transformed host cells, methods for
 CC identifying tissues and cells that express Nan, methods for
 CC identifying agents that modulate Nan channel activity or Nan
 CC channel mRNA transcription or translation, and a method for using
 CC such agents to treat acute or chronic pain, anaesthesia and
 CC hyperexcitability phenomena. The preferential expression of Nan in
 CC sensory DRG and trigeminal neurons provides a target for
 CC selectively modifying the behaviour of these nerve cells while not
 CC affecting other nerve cells in the brain and spinal cord. The
 CC gene is named SCN11a.
 XX
 SQ Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 1 other;

Query Match 34.8%; Score 2050.8; DB 20; Length 3638;
 Best Local Similarity 74.3%; Pred. No. 0; Mismatches 822; Indels 132; Gaps 8;
 Matches 2756; Conservative 0;

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RESULT 11

AAF57009

ID AAF57009 standard; cDNA; 6344 BP.

XX AAF57009;

XX 14-MAY-2001 (first entry)

XX Rat PN3 cDNA sequence.

Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;
tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; rat;
sodium channel protein; peripheral nervous system; allodynia; neuropathy;
hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnery;

XX analgesic; anti-HIV; ss.

XX Rattus sp.

XX

Db 1495 gtcttcaggaaagcagcgaggtgacacgagcagtggtgtctccacttcgcagcgcacagcca 1554
QY 1552 gtgagatctt----- 1562
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Qy	4119	cttaaaatgatattatcatgatggctgaaatctgcgcagacagcccaagaatgtgaagaaac		4178
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Qy	4179	ctttgatatcctcaacatagccttcgttggtcatctttacatatagatgctctcaataagt		4238
Db	4546	tctgggcagaaacaacaggtcttttggcgtcttcacggcggtggtgtgataagat		4605
Qy	4239	ctttgctttgaggcaacactcttcaccaatggctggaacttattgatitgtgtgctcgt		4298
Db	4606	gttcgccttcgcagactcatcttcaccaacggctcggaaacgtctcagactcatagtcgt		4665
Qy	4299	ggttctttctcatcattagtaacctcgtttt-----	cccgcttgaggagacagtgacattctctt	4355
Db	4666	gatccgttcattgggagctcgtcgtgtttcttgcaatccttaagtcaactggaacactact		4725
Qy	4356	cccgccaacgctctcagagctcgtccgcttggtcgtgattggtcgaaatcctcaggtcgt		4415
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[illegible]

RESULT 12
AAT77806
TD AAT77806 standard; cDNA; 6527 BP.

ΔΔ DE CDNA encoding variant rat DRG (SNS-B) #3.

Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
 Ax
 kW
 modulator; impulse; sensory neuron; acute pain; chronic pain;
 kW

neuropathic pain; glia; muscle; parasympathetic nervous system;
enteric nervous system; central nervous system; dorsal root ganglia;
cranial ganglia; ss.

Rattus rattus.

Key Location/Qualifiers
CDS 204..6602
FT /tag= a
FT /product= Variant_Rat_DRG(SNS-B)
FT 299
FT /tag= b
FT /label= C>G
FT 1092
FT /tag= c
FT /label= G>A
FT /note= "Causes Val > Ile substitution"
FT 1096
FT /tag= d
FT /label= C>T
FT /note= "Causes Ser > Phe substitution"
FT 1964
FT /tag= e
FT /label= G>C
FT 1965
FT /tag= f
FT /label= C>G
FT /note= "Causes His > Asp substitution"
FT 2472
FT /tag= g
FT /label= A>T
FT /note= "Causes Thr > Ser substitution"
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FT /tag= i
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FT /note= "Causes His > Arg substitution"
FT 3158
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FT /label= C>T
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FT /label= T>G
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FT 6525..6527
FT /tag= n
FT /note= "Addition of AAA"

WO9701577-A1.

16-JAN-1997.

25-JUN-1996; 96WO-GB01523.

28-JUN-1995; 95GB-0013180.

(UNLO) UNIV COLLEGE LONDON.

AKopian AN, Wood JN;

WPI; 1997-100165/09.

P-PSDB; AAW21740.

XX
PT
PT
PT
XX
XX
PS
XX

New isolated mammalian sensory neuron sodium channel protein - used to identify modulators of the sodium channel, partic. for the treatment of pain

Claim 9; Page 85-93; 128pp; English.

The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (para)sympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This sequence contains 12 nucleotide differences to the wildtype rat DRG(SNS-B) (see also AAT77803) causing nine amino acid changes.

Sequence 6527 BP; 1542 A; 1863 C; 1663 G; 1459 T; 0 other;

Query Match 23.8%; Score 1405.2; DB 18; Length 6527;
Best Local Similarity 57.5%; Pred. No. 0;
Matches 3246; Conservative 0; Mismatches 1923; Indels 477; Gaps 21;

QY 45 gaagatggagagaggtactaccggtgatatctctcccgagcagcgaggaattccgccctt 104
DB 191 gaagaatgagaagatggagctcccttgcgtcggtggaactaccatttcagcgtt 250
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DB 251 cacttcagatcactgagagatcgaagagcagattgctgctccacccggcagc 310
QY 165 gtccaaagacagcgcgagctgagctcc-----agctcgctcagcttga 212
DB 311 gcccagaaccaagacag 370
QY 213 cctaaaggcctccaggaagtactaagcttattgtgacattccctcagctgtgtac 272
DB 371 ctfgaaagactgtaaccagctgcccaagtctctatggtgagctccagcagactggtcgg 430
QY 273 gaacctctgagagacctgacccctactacaaagacacataagacacatcattggttga 332
DB 431 ggagccctggagagacctgagacctctctacagacacacagacacattcattggttga 490
QY 333 caagaaagacaaatttctgcttcagcgagcggtctgttcttccttggggtctt 392
DB 491 taaagcagagaccatttccagattcagtcacacttgggctgtggtcttcagctccct 550
QY 393 taatccctcagaagcttaattgattcttatctctgtccattcagcttcttagcttcat 452
DB 551 caacctgatcagaagaacagccatcaaatgctgtctccattcctggttctccattcat 610
QY 453 catctgcaggtgatcatcaatgattgctgaggaattctatgagagagaatttcga 512
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 Db 5267 cggctcccggggaactcgggagccgcggtggcagatcatcttctcaccactacat 5326
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 QY 4872 ggtctgggagaagtgtgacccccgagcgctgcagttcatccagttattcggccctctctga 4931
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 ID AAT77803 standard; cDNA; 6524 BP.
 AC AAT77803;
 XX
 XX 09-OCT-1997 (first entry)
 DT
 DE cDNA encoding wild type rat DRG (SNS-B).
 XX
 KW Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
 KW modulator; impulse; sensory neuron; acute pain; chronic pain;
 KW neuropathic pain; glia; muscle; parasympathetic nervous system;
 KW enteric nervous system; central nervous system; dorsal root ganglia;
 KW cranial ganglia; ss.
 XX
 OS Rattus rattus.
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 FH Key Location/Qualifiers
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 FT /*tag= a
 FT /product= Rat_DRG (SNS-B)
 XX
 PN W09701577-A1.
 XX
 PD 16-JAN-1997.
 XX
 PF 25-JUN-1996; 96WO-GB01523.
 XX
 PR 28-JUN-1995; 95GB-0013180.

(UNLO) UNIV COLLEGE LONDON.

Akopian AN, Wood JN;

WPI; 1997-100165/09.

P-PSDB; AAW21737.

New isolated mammalian sensory neuron sodium channel protein - used
 to identify modulators of the sodium channel, partic. for the
 treatment of pain

Claim 9; Page 50-58; 128pp; English.

The sequences given in AAT77803-06 encode the wild type and three
 variant forms of a rat sensory neuron sodium channel protein which
 is insensitive to tetrodotoxin. The proteins can be used for
 identifying modulators of the sodium channel. Blockers of the
 sodium channel will block or prevent the transmission of impulses
 along sensory neurons and thereby be useful in the treatment of acute,
 chronic or neuropathic pain. The novel protein is found only in sensory
 neurons and not in glia, muscle or the neurons of the (para)sympathetic,
 enteric or central nervous system. The protein is found preferably in
 the neurons of the dorsal root ganglia or cranial ganglia.

Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T; 0 other;

Query Match 23.7%; Score 1399; DB 18; Length 6524;

Best Local Similarity 57.6%; Pred. No. 0;

Matches 3251; Conservative 0; Mismatches 1915; Indels 483; Gaps 22;

QY 45 gaagatggagagaggtactaccggtgatcttcccgagcagcggaatttccgccccct 104

Db 191 gaagaatgagaagatgagctcccccttgcgtcgtgggaactaccaatttcagacggtt 250

QY 105 cacttcgactctctgctgccataaagaagcgaggtgctatccaa-----aa 152

Db 251 cactccagagtcactggcagagatcgagaagcagattgctcaccgcgcagccaagaa 310

QY 153 ggagaggaagaagtcctcaagacagcgagctgagccccagcctcgccctcagctga 212

Db 311 ggcagaaaccaagcacagagagagagggaggaagggcgagaaagccggcctcagctgga 370

QY 213 cctaaaggcctcagggaagtactacagcttattggtgacattccccctcagctgtttac 272

Db 371 ctgaaagactgtaaccagctgccaaagtctatggtgagctcccgagacagacggtcgg 430

QY 273 gaaacctctggagacacctggacccctactacaaagacacataagacattcatggtgtgaa 332

Db 431 ggagccctggagacctagaccttctctacagcacacacggacattcatggtgtgaa 490

QY 333 caagaaagaacaatttatcgcttcagcgcaagcgccctgttctcctcgtgggccccctt 392

Db 491 taaaagcagaccattcccgatcagtcgcaactggggccctggtgctctcagctccct 550

QY 393 taatccccctcagaagcttaattgattctctctcctcattcagctctttagcatttcat 452

Db 551 caacctgatcagaagaacagccatcaaaagtgtctgtccattcctggttctcattcat 610

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QY 513 caacgacattccggaatacgtcttctcattgggatttatattttagaagctgtgataaaat 572

Db 659 tccagagaaagtcagtcacttctcactgtctattacaccttcgaggtctgtgataagat 718

QY 573 attggcaagaggtctcattgttgatgagtttctcctcctcagacgtcggtgaactggtc 632

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QY 633 ggacttctatgtcatttggaacagcgatcgcaactgttttccggggcagccaagtaactct 692

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RESULT 14

AAF57016

ID AAF57016 standard; cDNA; 5874 BP.

XX AC AAF57016;

XX DT 14-MAY-2001 (first entry)

XX DE Human hPN3 cDNA sequence.

XX KW Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;

XX KW tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; human;
 XX KW sodium channel protein; peripheral nervous system; allodynia; neuropathy;
 XX KW hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnery;
 XX KW analgesic; anti-HIV; ss.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX CDS 1..5871
 XX FT /*tag= a
 XX FT /product= "hPN3"

US6184349-B1.

XX

PD 06-FEB-2001.
 XX 15-APR-1997; 97US-0843417.
 XX 11-OCT-1995; 95US-0511828.
 XX (SYNT) SYNTEX USA INC.
 XX Herman R, Delgado SG, Fish LM, Sangameswaran L, Robert DK;
 XX WPI; 2001-202004/20.
 XX P-PSDB; AAB61996.
 XX New rat and human tetrodotoxin-resistant, voltage-gated sodium channel
 XX proteins, present in peripheral nerve tissue, useful as a therapeutic
 XX target for compounds treating peripheral nervous system disorders -
 XX Disclosure; Fig 5A-K; 86pp; English.
 XX The invention provides purified and isolated rat and human peripheral
 XX nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins.
 XX The rat peripheral nerve sodium channel type 3 (PN3) protein or its human
 XX homologue are useful for the development of antibodies against PN3 which
 XX are useful in affinity chromatography to purify recombinant sodium
 XX channel proteins or polypeptides, or as a research tool. The PN3 proteins
 XX are useful as therapeutic targets for compounds to treat disorders of the
 XX peripheral nervous system such as allodynia, hyperalgesia, diabetic
 XX neuropathy, traumatic injury and acquired immunodeficiency syndrome
 XX (AIDS)-associated neuropathy. The present sequence represents the cDNA
 XX encoding the human hPN3 protein.
 XX Sequence 5874 BP; 1434 A; 1553 C; 1428 G; 1459 T; 0 other;

Query Match 23.5%; Score 1384.4; DB 22; Length 5874;
 Best Local Similarity 57.3%; Pred. No. 0;
 Matches 3227; Conservative 0; Mismatches 1956; Indels 477; Gaps 21;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 17:52:20 ; Search time 177.56 Seconds
(without alignments)
7521.631 Million cell updates/sec

Title: US-09-646-224A-1

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Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1384.4	23.5	5874	4	US-08-843-417-9
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4	1168.4	19.8	6007	3	US-09-024-0208-2
5	1168.4	19.8	6556	3	US-09-024-0208-7
6	1168.4	19.8	6586	3	US-09-024-0208-43
7	1156.8	19.6	6826	3	US-09-024-0208-8
8	1108.8	18.8	6452	3	US-08-836-325-9
9	1017.6	17.3	6371	3	US-08-836-325-13
10	1017.6	17.3	6404	3	US-08-836-325-14
11	866.2	14.7	3033	3	US-08-836-325-1
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13	676.6	11.5	6513	1	US-08-338-702-7
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17	676.6	11.5	6513	5	PCT-US95-14378-7
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26	368.4	6.2	930	3	US-08-605-284B-2
27	292.2	5.0	702	4	US-08-843-417-3

28	269.6	4.6	1237	2	US-08-808-793-26
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44	164.4	2.8	7266	3	US-09-452-007-1
45	149.8	2.5	5438	4	US-08-456-200B-5

ALIGNMENTS

RESULT 1
US-08-843-417-1
Sequence 1, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sandameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843.417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: Dorsal root ganglia
CELL TYPE: Peripheral nerve
US-08-843-417-1

Query Match	23.9%	Score 1411.4	DB 4	Length 5344	
Best Local Similarity	57.6%	Pred. No. 0			
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DB	3571	atcttcgggaanaacctgcttctcatctgtggacacacaaatgggttgagaccttcatactc	3630
QY	3172	tttgttattctgtgacgagtgagcgtgatatttgaagatgtcaactccccacgccgg	3231
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QY	3232	ccccaaattgagaattactaaggtgtacagataattttcaatttatttctctctgt	3291
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DB	4111	gaaatcgcatattgtcaacaaataaacccgactgtgagacgtcatggaggcgacacgacg	4170
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DB	4291	cgaaagccagacgacgacgcttgcactacgagggaacatctacatgtatcatcttacttcgctc	4350
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Best Local Similarity 60.3%; Pred. No. 8.2e-295;
Matches 225; Conservative 0; Mismatches 1346; Indels 119; Gaps 13;

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[illegible]

RESULT 5
US-09-024-020B-7
; Sequence 7, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,020B
; FILING DATE: 16-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-3097
; TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 7:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ. ID. NO. 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6826 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-024-020B-8

Query Match 19.6%; Score 1156.8; DB 3; Length 6826;
Best Local Similarity 60.2%; Pred. No. 9.4e-292;
Matches 2211; Conservative 0; Mismatches 1342; Indels 119; Gaps 13;
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RESULT 14

US-08-337-339-7

Sequence 7, Application US/08337339

Patent No. 5593864

GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.

APPLICANT: Hall, Linda

APPLICANT: Peng, Gouping

APPLICANT: Van Der Ploeg, Leonardus

TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

TITLE OF INVENTION: PARA SODIUM CHANNEL

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESSES:

ADDRESSEE: John W. Wallen III

STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CITY: New York, New York

Db 4080 ATGACAGAAATATTACGGGTATATTCTTGGAAATGTTAATCAAGTGGTGGCGCTC 4139
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RESULT 15

US-08-724-095-7

Sequence 7, Application US/08724095

Patent No. 5688917

GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.

APPLICANT: Hall, Linda

APPLICANT: Feng, Gouping

APPLICANT: Van Der Ploeg, Leonardus

TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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12529.730 Million cell updates/sec

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Perfect score: 5897

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Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST

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IMAGE:4316490 5', mRNA sequence.

BG694370

GI:13953218

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 650)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Unpublished (1997)

Tumor Gene Index

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

CDNA Library Preparation: M. Bento Soares Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: infoimage.llnl.gov

MG1:1597258

Seq primer: T7 primer.

Location/Qualifiers

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/dev_stage="embryo, 14 dpc"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pT73D-Pac; Site_1: NotI;
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5'-AATCGGAAGAAATTCGGCGCGCGCGCTTTTCTTTTCTTTT-3';
double-stranded cDNA was ligated to EcoRI adaptors
5'-AATCGCGACGAGG-3' AND 5'-CTCGTGGCG-3' (Pharmacia).
digested with NotI and cloned into the NotI and EcoRI
sites of the pT73D-Pac vector. Library went through one
round of normalization, and was constructed in the
laboratory of M. Bento Soares (University of Iowa)."
BASE COUNT 153 a 181 c 151 g 165 t
ORIGIN

Query Match 9.2%; Score 541.2; DB 11; Length 650;
Best Local Similarity 89.5%; Pred. No. 3.7e-100;
Matches 582; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
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QY 4584 cttcgagacctttacgggcagcatgctgctctctccagataaccacttcgctgctg 4643
Db 61 CTTTGACACTTTCGGGCGACATGCTGCTCTCTCCAGATACACACTTCAGCGGGCTG 120
QY 4644 ggataacctctcaacccccatgctggaggcaaaagaacactgcacactctctcccaaga 4703
Db 121 GGATGCTCTCTCAACCCCATGCTGGAATCAAAAGCCTTTTGCAATCTCTCTCCCAAGA 180
QY 4704 cagctgtcagcagcagatagcgtgctgctacttacttcagttacatcatctctctt 4763
Db 181 GAGTGTGACAGCGCGCAGATAGCATAGTCTACTCTGTCAGCTACATCATCTCTCT 240
QY 4764 cctcatcgtgtcaacatgtacatgctgctgctcctcgagaaacttcaacacagccagga 4823
Db 241 TCTCATGTGTTAAATGATACATAGCTGTGATCTTAGAGAACTTCAACAGCCACAGA 300
QY 4824 ggagagcaggacctctggagaggacgactttgaaattcttatgaggtctgggagaa 4883
Db 301 GGAGAGCGAGACCCCTTGGCGAAGACGACTTTGAGATCTCTATGAGATCTGGGAGAA 360
QY 4884 gtttgacccgagcgtcgcagttcatccagatttcggccctctctgactttggcagc 4943
Db 361 GTTTGACCCGAGCAACACAGTTTCAATCCAGTACTCATCTCTCTGACTTCGCGCAGC 420
QY 4944 cctgcccggagcgttgcgtgtggccagccgaaataaagtcttcagtcttagtgagactt 5003
Db 421 CTTGCCCGAGCGTGTGCTGTGGCCAGCCCAACAGGTTTCAGTTCTCATGTGGACTT 480
QY 5004 gccatggtgatggcgacgcctccatttgcattggtatgtttcttcttcttccactaccag 5063
Db 481 GCCCATGCTGATGGGTGATCGCTTCCATTCGATGCATGATGCTCTCTCTGCTTCCACCAC 540
QY 5064 ggtcctcgggactccagcgttgatcaccatgaaacatgatggaggagaagtattat 5123
Db 541 GGTCTCGGAACCTCCAGCGCTTGGATACCATGAAAGCCATGATGGAGGAGAAGTTTCAAT 600
QY 5124 ggaggccaaaccttttaagaagctctacgagcccatagtaccaccacca 5173
Db 601 GGAGGCCAATCTTTCAAGAAGTTGTACGAGCCCATGTTCAACCCACCA 650

RESULT 2
BF980111/c
LOCUS BF980111 892 bp mRNA EST 23-JAN-2001
DEFINITION 602288113T1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4373859 3',
mRNA sequence.
ACCESSION BF980111
VERSION BF980111.1 GI:12347326

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-NCBI http://mgc.nci.nih.gov/
1 (bases 1 to 892)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10036 row: j column: 04
High quality sequence start: 13
High quality sequence stop: 729.
Location/Qualifiers
1..892
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4373859"
/clone_lib="NIH_MGC_97"
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/note="Organ: testis; Vector: pBluescriptR (modified
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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to R0.5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI), National
Institutes of Health). Note: this is a NIH_MGC Library."
EASE COUNT 207 a 213 c 214 g 258 t
ORIGIN

Query Match 8.2%; Score 485.4; DB 11; Length 892;
Best Local Similarity 81.7%; Pred. No. 8.5e-89;
Matches 609; Conservative 0; Mismatches 131; Indels 5; Gaps 4;
QY 1105 caagactcctggagaggtttaccgacagatcctggacacctgtggtactacttgc 1164
Db 750 CCAGATTCTTGGGAGAAGCCTTATCAACAGAACCTGCGTA-CTACGGGCTCTACTCAGTC 692
QY 1165 ttcttctcgtgggtgcatct-tcctgggctcttcttaaccttaacctgac 1223
Db 691 TTCTTCTCATGTGGGTCAATTTGCTGGGCTCCATCTACCTGATTAAC--TAACCTGGC 634
QY 1224 tgtgtccaccatgcttattgaagacagacagaaatgtagctgtgacagagggccaa 1283
Db 633 TGTGTGTACCATGTCATATGAGGAGCAGAACAAAGATAGTAGAGGCCAA 574
QY 1284 ggagaaatgttccaggaagcccgagcgtgttaaggagaggaaggaggtcctgggtgc 1343
Db 573 GGAAGAAGATGTTTCAGGAAGCCAGCAGCTGTTAAAGGAGGAGGAGGCTCTGGTTGC 514
QY 1344 catgggaattgacagaagttcccttaattccctcaagcttcacctttccccaagaa 1403
Db 513 CATGGGAATTGACAGAAGTTTACTTCTTCTTGAACATCATATTTATCCCAAAAAA 454
QY 1404 gaggaagtcttccgttagtaagacaagaagctcttcttattgagaggtccaaagcgc 1463
Db 453 GAGAAAGCTCTTTGGTAAATAGAAAGAAAGTCTCTTTTGTAGAGAGTCTGGGARA 394
QY 1464 ccaagcctcagcgtctgattcagaggacga-tgctcttaaaaaatccacagctccttgagc 1522
Db 393 CCAGCCTCCTGGGTGAGATTCTGTATGAAGATTGCCAAAAAAGCCACAGCTCCTAGAGC 334

REFERENCE 1 (bases 1 to 615)
 AUTHORS Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Stepcioe,M., Underwood,K., Theising,B., Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE WashU Zebrafish EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: fl13c05.x1
 Contact: S.L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center
 Seq primer: T3 ET from Amersham
 High quality sequence stop: 467.
 Location/Qualifiers
 1. .615
 /organism="Danio rerio"
 /strain="AB"
 /db_xref="taxon:7955"
 /clone_lib="Sugano Kawakami zebrafish DRA"
 /sex="mixed (one male and one female, including unfertilized eggs)"
 /dev_stage="adult"
 /lab_host="DH10B (phage resistant)"
 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGATG); Site_2: DraIII (CAGCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTGTGGCTACTG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGATG, 3' site CAGCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGTGGC and 3' end primer CGACCTGCGAGCTCGACACA."
 BASE COUNT 155 a 156 c 158 g 146 t
 ORIGIN

Query Match 4.8%; Score 283.4; DB 10; Length 615;
 Best Local Similarity 67.9%; Pred. No. 1.9e-47;
 Matches 414; Conservative 0; Mismatches 196; Indels 3; Gaps 1;
 QY 3535 tgctcatttctgctcgtatttctgtggtgagtaatttatttctggaagt 3594
 Db 2 TGCTGATCTCTGGCTCACTCAGCATTTATGGGGTCAATCTGCTGGTGAAGTTT 61
 QY 3595 ggaaggtgcattaacggggacaga---cataaatatgtattgttttaaccgaagtccg 3651
 Db 62 GGCGCTGCTGTAACCGGACGGGTTTCATCTATAATCTCTGACATCAACACCGCAGC 121
 QY 3652 aaccgaagcaatgaataactagtaattactgtggaaggtccgcaggtcaactttgac 3711
 Db 122 GAGTGTCTGGAGTGAACAGCAGCAGCAGTATTACTGGACCAAGTAAGTTAATTTCCGAC 181
 QY 3712 aacgtgggaatgctatctcgccctgctgaagtgcacacctataagggctgctgaa 3771
 Db 182 AACGTGGCGCTGGATATCTCGCGCTGCTGCAAGTGCCACAGTTTAAGGCTGGATGGAG 241
 QY 3772 atcatgaatgctgctgattccagagagaagacagcagcgacttttgaggcaac 3831
 Db 242 ATCATGTACCGCGCTGGAGCTCGAGAGCTGTGGAGGACCAACCAATCAAGGAAACAGC 301
 QY 3832 ctctacgcgtatctctactttgtgtttttatcatctctggtctctcttaacctgaac 3891
 Db 302 CTGTACATGTACCTGACTTCTGTCATCTTTCATCTCTCGCTCTCTTCTTTACCCCTAAC 361

QY 3892 cttttatcgggtgtattattgacaaacttcaatcagcagcaaaaaagttagggtggccaa 3951
 Db 362 CTGTTCATCGGTGTGATCATCGCAACTTCAACCAAGAGAGAAAGTTAGGGGGGCAG 421
 QY 3952 gacattttatgacagagaacagaataattacaaatgcaatgaaagaagttagggaac 4011
 Db 422 GACATCTTCATGACCGAAGAGAGAGAATAACTACACGCCCATGAGAAACTGGGCTCC 481
 QY 4012 aagaaacctcaaaagcccatcccaagccctgaacaaaatgtcaagcctttgtgttgac 4071
 Db 482 AAGAAGCACAGAGAGCCCATACACCAAGACCAACCTGCCAGGGCTTCTTCTTCGAC 541
 QY 4072 ctggtcacagccaggtctttgacgtcatcattctggtgtttattgtcttaaatatgatt 4131
 Db 542 CTGCTGTCCAGCAGGGGTTTGACATCTCATCATGCTGCTGATCATCTCTGAATATG 601
 QY 4132 atcatgaggtcg 4144
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 RESULT 5
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 LOCUS 602374246F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481819 5',
 DEFINITION mRNA sequence.
 ACCESSION BG342331
 VERSION BG342331.1 GI:13148769
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 674)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-f@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAMI0317 row: 1 column: 12
 High quality sequence stop: 672.
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 1. .674
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 /db_xref="taxon:10090"
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 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
 BASE COUNT 146 a 167 c 161 g 200 t
 ORIGIN

Query Match 4.5%; Score 266.6; DB 11; Length 674;
 Best Local Similarity 65.6%; Pred. No. 3.9e-44;
 Matches 405; Conservative 0; Mismatches 209; Indels 3; Gaps 1;
 QY 4061 ttgtgttcagcctggttcacagccaggtctttgacgtcaatctgtggtttattgtct 4120
 Db 5 TGGTTTTTGACTTTGTAACCAAGCAAGTGTGTGATATACAGCATCATGATCTCATCTGTC 64


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QY 4121 taaatgattatcatgagtgctggaatcgtccgaccagcccaagaagtgtgaagaaaccc 4180
D 65 TGAACATGTTGACCATGATGGTGAAGAACGATGACCAAGCGGATTTATGTACAAAGCATTT 124
QY 4181 ttgatattcctcaatagccttgctggtcatcttaccatagagtgctcatcaaatgctc 4240
D 125 TGTACGCGATCAACCTGGTGTCTGCTGCTGTTACCGGCGAGTGTGCTCAAGCTCA 184
QY 4241 ttgctttgaggcaactcctcaccatggctgggaactatttattggttggtgctggtg 4300
D 185 TCTCGCTCCGCCATTATTATTCACCATTTGGATGGAAACATTTTCGATTTTGTGGTCA 244
QY 4301 ttcttttatcatatgataccctggtttccogcttggagacagtacatttctccogc 4360
D 245 TCTCTCCCATTTGAGGAGATTTCTTTCGCGAGCTAATAGAAA---AGTATTTTGTGCTC 301
QY 4361 ccaagctcttcagagtcgctcgttgcctgctgattggtggaatcctcaggctggtcgg 4420
D 302 CTACCTCTGTTCCGAGTATCCCGCTGGCAGGATTGGACGAATCTTACGCTGTGATCAAG 361
QY 4421 ctgcccgggaatcaggacctcctcttctgcttgatgctctcctccctctctcttca 4480
D 362 GTCCCAAGGGATCCCGACGCTGCTTCTGCTGTGATGATGCTCCCTCTGCGCTGTTTA 421
QY 4481 acatcggctgctgctctctctctggtggtgatttcatcgcattcttgggagtgagctggt 4540
D 422 ACATCGGCTCCTGCTCTTCTGCTCATGTTTCATCTACGCCATCTTTGGGATGTCCAAC 481
QY 4541 ttctccaaagtgaagaaggctcgggagtcagacagacattctcacttcgagaccttacgg 4600
D 482 TTCCCTATGTTTAAGAGGGAAGTTGGGATTTGATGACATGTTTCAACTTTGAGACCTTC 541
QY 4601 gcaagctgctgctcctctccagataaccacttcgctgctggtggtgataccctcctca 4660
D 542 ACAGCATGATCTCCCTGTTTCCCAATCACCACCTCTCGGGCTGGGATGGAGTCTGTCGCC 601
QY 4661 ccatgctgagggcaaaa 4677
D 602 CCATCCTCAAAAGGAAA 618

RESULT 6
BE550573/c
LOCUS
DEFINITION
7a29e10.x1 NCI-CGAP_G66 Homo sapiens cDNA clone IMAGE:3220170.3'
similar to TR:088457 O88457 VOLTAGE-GATED NA CHANNEL ALPHA SUBUNIT
NAN., mRNA sequence.
ACCESSION BE550573
VERSION BE550573.1 GI:9792265
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 690)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 456.

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FEATURES
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                /lab_host="DH10B"
                /note="Vector: pT73D-Pac (Pharmacia) with a modified
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                from the normalized library NCI-CGAP_G64 was prepared, and
                ss circles were made in vitro. Following HAP purification,
                this DNA was used as a tracer in a subtractive hybridization
                reaction. The driver was PCR-amplified cDNAs from a pool
                of 5,000 clones made from the same library (clones IDs
                1257096-1258631, 1469064-1470983, and 1475592-1476743).
                Subtraction by Bento Soares and M. Fatima Bonaldi."
            BASE COUNT 180 a 151 c 160 g 199 t
            ORIGIN
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                D 411 ACAGCTCATAGAGCAACCAACGACTGTCCAGAAATCTATCACTGGACCACTTTGATGA 352
                QY 1569 gcactgagccccctccacagggcagagagcgctgagcgtgtcagtgatcttaaccatcac 1628
                D 351 GCATGGAGATCCTCTCTCAAGAGGAGAGAGCAGCTGCTGCTGAGCATCTCCACATCAC 292
                QY 1629 catacagggaacgaataattccaggagcctgtttcccatgtgggaaaaatttggcctc 1688
                D 291 CATGAGGGAACAGAAATAATCAAGAGACCTTGTCTCCCTTGGGAGAAACCTGGGCATC 232
                QY 1689 taagtacctgtgtggtgactgtagcctcagtgctgtgcataaagaagctcctgcggac 1748
                D 231 CAAGTACCTGTGTGGAACCTGTGCCCCAGTGGCTGTGCTGTAGAGAGGCTCTGAGAAC 172
                QY 1749 catcatgaaggatcccttactgagctggccatcacatcatcatcatcatcaatccgt 1808
                D 171 TGTGATGACTGACCCGCTTTACTGAGTGGCCATCACCATGTGCATCATCATCAACACTGT 112
                QY 1809 ttcttiagcgtgagacacacacacacatggtgatacaacttaaacaccatactgaaatagg 1868
                D 111 CTGTGTCGCATGGAGCATCAAGATGGAGGCCAGTTTGTGAGAAAGATGTTGAATATAGG 52
                QY 1869 aaactgggt 1877
                D 51 GAATTTCGT 43

RESULT 7
BE550573
LOCUS
DEFINITION
225823 MARC 280V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE550573
VERSION BE550573.1 GI:10869999
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 561)
REFERENCE
    Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
    Casas,E., Wray,J.E., White,J., Cho,J., Fahrnkruug,S.C., Bennett
    G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
    Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
    Keele,J.W.
    Sequence evaluation of four pooled-tissue normalized bovine CDNA

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RESULT 15

CNS04HC1/c

LOCUS

DEFINITION

CNS04HC1 501 bp DNA GSS 21-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
110M19 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

AL290746

VERSION

GI:8029326

KEYWORDS

GSS: genome survey sequence.

SOURCE

Tetraodon nigroviridis.

ORGANISM

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE

1 (bases 1 to 501)

AUTHORS

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

TITLE

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 501)

AUTHORS

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

TITLE

Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

JOURNAL

Unpublished

REFERENCE

3 (bases 1 to 501)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1..501

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/db_xref="taxon:99883"

/clone_lib="G"

/notes="Genoscope"

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BASE COUNT

ORIGIN

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Best Local Similarity 3.7%; Score 220.8; DB 13; Length 501;

Matches 317; Conservative 15; Mismatches 138; Indels 2; Gaps 2;

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Qy 4749 catcatcatctctctctcatcgtggtcaacatgtacatcgtgtgatctcgcgagaactt 4808

Dy 413 CATCATCATCTCTCTTTCTTATCGTGGTCAACATGATCATGCCCATCATCTCGGAGAACTT 354

Qy 4809 caacacagc-cacgagagagagagaccctctggagagagagactttgaaatctct 4867

Dy 353 MAGCGTGGCAACCGAGGAGAGACCCGAGCTCTGAGGGAGAGAGATTCGAGATGTCT 294

Qy 4868 atgaggtctggagaagttgaccccgagcgtcgcaggttcatccagttattcggccctct 4927

Dy 293 ACGAGGTGTGGGAGAAGTTCGACCGGAGGCAACGCGAGTTAATDAGGTACGCCAAGCTGT 234

Qy 4928 ctgactttggagacgcctcgcgagcgttgctgtggccaaagcgaataagttcagtt 4987

Dy 233 CGGACTTCGCGGACTCTCTGTGGGAMMG-TGCGCATCGCVAAACCCMAAAAGATAAGC 175

4988 ttctagtgtgacttgccttgccttgatggcgacccgctccattgcattgcatgattctct 5047
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5108 tggagagagaagtattatggaggcccaacccttttaagaagctctacgagcccat 5159
54 TGGAGGAGAAGTTTCATGATGATGGCCCAACCCCTCAAAGATATWCATAGAGCCAAT 3

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2002, 22:39:30 ; Search time 76.96 Seconds
(without alignments)
1698.796 Million cell updates/sec

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Perfect score: 9173
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT.*
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10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9173	100.0	1765	AAV41668	Rat sensory neuron
2	9153	99.8	1765	AAV16572	Type 5 sodium chan
3	9149	99.7	1765	AAV06596	Rat sodium channel
4	9149	99.7	1765	AAV20122	Rat sodium channel
5	9141	99.7	1765	AAV20123	Rat sodium channel
6	8153	88.9	1765	AAV06597	Mouse sodium chann
7	8153	88.9	1765	AAV20124	Mouse sodium chann
8	6709	73.1	1791	AAV20121	Human sodium chann
9	4712.5	51.4	2016	AAV23994	Human hhl sodium c
10	4712	51.4	2015	AAV23994	Human SCN5A mutant
11	4711.5	51.4	2016	AAV23994	Human SCN5A protei

12	4711.5	51.4	2016	22	AAV22240	Human SCN5A mutant
13	4711.5	51.4	2016	22	AAV22245	Human SCN5A mutant
14	4708.5	51.3	2016	22	AAV22241	Human SCN5A mutant
15	4708.5	51.3	2016	22	AAV22244	Human SCN5A mutant
16	4704.5	51.3	2016	22	AAV22243	Human SCN5A mutant
17	4671	50.9	2020	11	AAV06584	Cardiac sodium cha
18	4669.5	50.9	1956	22	AAV61996	Human peripheral n
19	4663	50.8	2019	16	AAV67913	Cardiac sodium cha
20	454.5	49.7	1957	18	AAV21740	Variant rat DRG (S
21	4553	49.6	1956	22	AAV61995	Rat peripheral ner
22	4541.5	49.5	1957	18	AAV21737	Wild type rat DRG
23	4541	49.5	1977	17	AAV99641	Peripheral nervous
24	4518	49.3	1962	20	AAV17250	NaNG polypeptide.
25	4513.5	49.2	1243	22	AAV20126	Human sodium chann
26	4513.5	49.2	1984	17	AAV99639	Peripheral nervous
27	4510.5	49.2	1243	20	AAV06598	Human sodium chann
28	4506	49.1	2005	22	AAV99677	Human neonatal for
29	4505	49.1	2005	22	AAV99676	Human adult form o
30	4500.5	49.1	1989	17	AAV92317	Peripheral nervous
31	4496	49.0	2009	22	AAV99674	Human adult form o
32	4480	48.8	2132	18	AAV21739	Variant rat DRG (S
33	4470.5	48.7	1951	22	AAV99679	Human neonatal for
34	4468.5	48.7	1233	22	AAV20125	Human sodium chann
35	4466.5	48.7	1951	22	AAV99678	Human adult form o
36	4394.5	47.9	1978	19	AAV69361	Tetrodotoxin-sensi
37	4390.5	47.9	1988	19	AAV69362	Tetrodotoxin-sensi
38	4390.5	47.9	1989	17	AAV99640	Peripheral nervous
39	4354	47.5	1980	21	AAV23563	Human sodium chann
40	4195	45.7	1835	17	AAV23316	Peripheral nervous
41	354.5	38.7	2105	19	AAV57772	Musca domestica vo
42	354.5	38.7	2105	20	AAV95777	Calcium permeable
43	3550.5	38.7	2104	19	AAV57773	Musca domestica vo
44	3550.5	38.7	2104	20	AAV95778	Calcium permeable
45	3532	38.5	2100	20	AAV95779	Calcium permeable

ALIGNMENTS

RESULT 1

AAV41668
ID AAV41668 standard; Protein: 1765 AA.
AC AAV41668;
XX
XX
DT 03-DEC-1999 (first entry)
XX
DE Rat sensory neurone specific 2a protein sequence.
XX
XX Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;
KW voltage gated; hypersensitivity.
XX
XX Rattus sp.
OS
XX
XX WO9947670-A1.
XX
XX 23-SEP-1999.
XX
XX 18-MAR-1999; 99WO-GB00838.
XX
XX 18-MAR-1998; 98GB-0005793.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Grose DT, Hick CA, Tate SN;
XX
XX WPI; 1999-562112/47.
XX
XX N-PSDB; AA221480.
XX
XX Mammalian sodium channel protein for treating pain and hypersensitivity
XX
XX Claim 1; Page 59-64; 73pp; English.

KW dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;
 KW diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
 KW neuropathic pain; migraine; headache.
 XX Rattus sp.
 XX FR2771103-A1.
 XX 21-MAY-1999.
 XX 19-NOV-1998; 98FR-0014551.
 XX 20-NOV-1997; 97US-0066225.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;
 XX WPT; 1999-315739/27.
 DR N-PSDB; AAX60241.
 XX
 PT Isolated DNA encoding sodium channel of the nervous system
 XX Claim 17; Fig 2A-F; 90pp; French.
 XX
 CC The present sequence represents a type 5 sodium channel protein
 CC designated PN5. The protein is a sodium ion channel of the
 CC nervous system, and is highly expressed in plexiform and dorsal
 CC root ganglia. The protein can be used to identify inhibitors of
 CC sodium channel proteins that are resistant to tetrodotoxin (TTX).
 CC The inhibitors are potentially useful for treating epilepsy,
 CC stroke, diabetic neuropathy, traumatic injuries, AIDS-related
 CC neuropathy, and especially neuropathic pain, e.g. migraine and
 CC headache.
 XX
 SQ Sequence 1765 AA;
 Query Match 99.8%; Score 9153; DB 20; Length 1765;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1760; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MEERYYPVFPDENRFRPFTSDSLAAIKKRIAIOEKRRKSKDAAAEPPQRPQLDLKASR 60
 DB 1 meeryyvpvfpdennrfrpftsdslaiekrilqekrkskdkaaepprpqldlkasr 60
 QY 61 KLPLKYGDIPELVTKPLEDLDPYKDKHTFMVLNKKRTIYRFSKAKRALFTLGFNPLRS 120
 DB 61 klplygdipelvkvpleldlpykdkhtfmvlnkkrtlyrfsakralflgfnplrs 120
 QY 121 LMIRISVHSVSMFIICVTIINCMMANSMERSFDNDIPEYVFIGIVILEAVIKILARGF 180
 DB 121 lmirishsvsmfiictvtiincmmansemersfdndipeyfigivileavikilargf 180
 QY 181 IVDFSEFLRDPWNWLDIVTGTATCPGQVNLASALRTPRPRALKAISVISGLKVIV 240
 DB 181 ivdfesflrpdwnwldivtgatcpqgvnlalsalrtprpralkaisvisglkviv 240
 QY 241 GALLRSVKKLVDMVNLVTLFCLSIIFALVGOQLFMGILNOKCIKHNCGNPNASNKDCFEKEK 300
 DB 241 gallrsvkkldvmvnlvltfclsiifalvgoolfmgilnqckikhncgpnasnkdcfekek 300
 QY 301 DSEDFIMCGTWLGRPCPNGSTCDKTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLY 360
 DB 301 dsedfimcgtwlgRPCPNGSTCDKTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLY 360
 QY 361 RQILRTSGIVFVFVFFVIFGSPYLLNLTAVVTMAYEONRNVAATEAKEKMFQEAQ 420
 DB 361 rqlirtsgivfvfVFFVIFGSPYLLNLTAVVTMAYEONRNVAATEAKEKMFQEAQ 420
 QY 421 QLLREEKALVAMGIDRSSLNLSQASSFSPPKKRFFGSKTRKSKFFMRGSKTAQASDSE 480
 DB 421 qlireekalvamgidrsslnlsqassfsppkkrrffgsktrkskffmrsgsktaqasds 480

481 DDASKNPQLLEQTKRLSONLPVDLFDHVDPLHRQRALSAYSILITITIQEKEQPCFP 540
 QY
 481 ddasknpqlleqtkrlsonlpvdlfdhvdplhrqralsavsiltitmqeqekfepcfcfp 540
 DB
 541 CGKNLASKYLWDCSPQWLCKIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHMDDNL 600
 QY
 541 cgknlaskylwdcspqwlckikvltimtqpfteaiticiciintvflavehnmddnl 600
 DB
 601 KTIKIGNWVFTGIFIAEMCKIIIALDPYHYFRHGNVDFDSIVALSLIADLYNTLSNN 660
 QY
 601 ktilkignwvftgifaemckiiialdpvyhyfrhgnvdfdsivalsladlyntlsnn 660
 DB
 661 RSFLASRLVRLVKLAKSWPTLNTLIKIHSGVAGALNLTIVVLITVVFIFSVGMRFGT 720
 QY
 661 rsflasrlvrlvklakswptlntlikihsgvagnltvltivvfifsvgmrflgt 720
 DB
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 QY
 721 kfnktatqbrprrrhmdnfyhsflvvrilcgewienmwgmqmdgspcliiivpl 780
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 QY
 781 imvigklvvlftallnlsfseekdglsetrktvolaldrfrrafspmlhalqsf 840
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 841 CCKCRRKNSPKPKETTESFAGENKDSILPDARPKKEYDTDMALYTGOAGAPLAEVE 900
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 841 cckcrrknsppkpkettesfagenkdsilpdarpkkeydtmalytgoagaplaeve 900
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 901 DDVEYCEGEGALPTSHSAGVQAGDLPPETKQLTSPDDQGVMEVFSEEDLHLSIQSPRK 960
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 961 KSDAVSMLESECTIDLNDIFRNLOKTVSPKQDRCPPKGLSCHFLCHTKDKRSPWVLW 1020
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 961 ksdavsmlesectidlndifrnloktvspkqdrccpklgschflchtkdkrspwvlw 1020
 DB
 1021 WNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLCRCNDNFTFTFL 1080
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 1021 wnirktcyqivkhswfesfiifvillssgalifedvnlpsrpqveklrcndnftftfl 1080
 DB
 1081 LEMILKWVAFGRFYFTSAWCWDLFLIVVSVLSLNMNPSLKSFRTLRALRALSQFE 1140
 QY
 1081 lemilkwvafgrfyftsawcwldflivvsvlslnmnlpsksftrlaralralsqfe 1140
 DB
 1141 GMKVVVVALISAIPAILNVLVCLIFWLVCILGNLPSFGKFGRCINGTDINMYLDFTEV 1200
 QY
 1141 gmkvvvvalisaipailnvlvclifwlvcilgnlpsfgkfgrcingtdinmyldftev 1200
 DB
 1201 PNRSCQNISNYSWKVPQVNFNDVGNAYLALLQVATYKGLRITMNAAVDSREKDEQDPPEA 1260
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 1201 pnrscqnishnyswkvpqvnfdvgnaylallqvatykgwleimnaavdsrekdeqdpfea 1260
 DB
 1261 NLYAYLVFVFIIFCSFTLMLFGIVIDNNOQKQLGGQDIFMTESQKYYNAMKKLG 1320
 QY
 1261 nlyaylvfvfiifcsftlmlfgiividnnoqkqlggqdifmtesqkyynamkklg 1320
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 1321 TKKPKQPIPRPLNKOAFVFDLVTQVFDVITILGLIVLNMIMMAESADQPKVKTFDI 1380
 QY
 1321 tkkpkqpiprplnkcoafvfdlvtqvfdvitilglivlnmimmaesadqpkvktfdi 1380
 DB
 1381 LNIAPVFIITIECLIKVFALRQHYFTNGWNLFDVCVVVLSIISTLVSRLESDISFPPTL 1440
 QY
 1381 lniafvfiitieclikvfallrqhyftngwnlfdcvvvvlsiistlvsrledsdisfpptl 1440
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 1441 FRVRLARIGIRLRLVRAARGIRTLFLFALMMSLSFLNIGLLFLVMPITYAIFGMSWFSK 1500
 QY
 1441 frvrlarigrilrlvraargirtllfalmmsslsflnigllflvmpityaifgmswfsk 1500
 DB
 1501 VKKSGIDDIINFETFTGSMCLCLFIQITTSAGWDTLNPNMLEAKHCNCSODSCQOPIA 1560
 QY
 1501 vkksgiddiinfetftgsmiclfqittsagwdtllnmpmleakehcnssodscqqpia 1560
 DB

Qy 1561 VYFVSXIIISFLIVNMVYIAVILENENTATESEDPAGEDDFEIFYEWEKFDPEASQF 1620
Db 1561 VVYFVSIIISFLIVNMVYIAVILENENTATESEDPAGEDDFEIFYEWEKFDPEASQF 1620
Qy 1621 IQYSALSDFDALPEPLRVAKPNKFOFLVMDLPMVMGDRHLHCDVLFATFTRVLGDSSGL 1680
Db 1621 IQYSALSDFDALPEPLRVAKPNKFOFLVMDLPMVMGDRHLHCDVLFATFTRVLGDSSGL 1680
Qy 1681 DTMKTMEEKPMEANPKKLYEPIVTTTKRKEEBOGAIVQRAYRKHKMKVVKLRLKDRS 1740
Db 1681 dtmktmeekpmeanpkklyepivtttkrkeeeogaaviqrayrkhkmmkvkrlrlkdrs 1740
Qy 1741 SSSHQVFCNGDLSSLDVAKVKVHND 1765
Db 1741 ssshqvcngdlssldvkvkvhnd 1765
RESULT 3
AAY06596
ID AAY06596 standard; Protein; 1765 AA.
XX
AC AAY06596;
XX
DT 26-OCT-1999 (first entry)
XX
DE Rat sodium channel NaN.
XX
KW NaN; sodium channel; ion transport; rat; dorsal root ganglia;
KW pain; paraesthesia; hyperexcitability; therapy.
XX
OS Rattus sp.
XX
PH Location/Qualifiers
FT Region 125..148
FT /label= DI-S1
FT /note= "domain I transmembrane segment S1"
FT Region 157..177
FT /label= DI-S2
FT /note= "domain I transmembrane segment S2"
FT Region 191..210
FT /label= DI-S3
FT /note= "domain I transmembrane segment S3"
FT Region 216..237
FT /label= DI-S4
FT /note= "domain I transmembrane segment S4"
FT Region 254..273
FT /label= DI-S5
FT /note= "domain I transmembrane segment S5"
FT Region 338..350
FT /label= DI-S51
FT /note= "domain I transmembrane segment S51"
FT Region 353..358
FT /label= DI-S52
FT /note= "domain I transmembrane segment S52, the
FT Ser-355 residue is implicated in the
FT TTX-R phenotype"
FT Region 371..398
FT /label= DI-S6
FT /note= "domain I transmembrane segment S6"
FT Region 567..591
FT /label= DII-S1
FT /note= "domain II transmembrane segment S1"
FT Region 603..624
FT /label= DII-S2
FT /note= "domain II transmembrane segment S2"
FT Region 633..654
FT /label= DII-S3
FT /note= "domain II transmembrane segment S3"
FT Region 663..682
FT /label= DII-S4
FT /note= "domain II transmembrane segment S4"
FT Region 699..719
FT /label= DII-S5

FT /note= "domain II transmembrane segment S5"
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FT /note= "domain IV transmembrane segment S5"
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FT /note= "domain IV transmembrane segment S52"
FT /label= DIV-S6
FT /note= "domain IV transmembrane segment S6"
XX WO938889-A2.
XX
XX 05-AUG-1999.
XX
XX 29-JAN-1999; 99WO-US02008.
XX
XX 20-NOV-1998; 98US-0109402.
XX 29-NOV-1998; 98US-0072990.
XX (UYA) UNIV YALE.
XX
XX Dlb-Hajj S, Waxman S;
XX WPI; 1999-479168/40.
XX N-PSDB; AAX87600.
XX
XX New isolated nucleic acids encoding sodium channels, used to develop
XX products for treating acute or chronic pain or hyperexcitability
XX phenomena

PS Claim 1; Fig 2A-C: 91pp; English:

This is the predicted amino acid sequence of the rat NaN channel, as deduced from isolated rat NaN cDNA (see AAX87600). NaN is a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord.

Sequence	1765 AA;
SQ	

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Query Match          99.7%; Score 9149; DB 20; Length 1765;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1759; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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Qy	1	MEERYYPVDPDNRPPFTSDLAALKKRIAIOKERKSKSKAAAEPOPRQOLDUKASR	60
Db	1	meeryypvfpdnerppftsdlaalekriaiokerkkskkaaepprqoldlksar	60
Qy	61	KLPLKYGDIPPELVTPLEDDPYVYKDHTEFWMLNKKRTYRPSAKRALFILGPNPLRS	120
Db	61	klplkygdipelvtpleddpyvkhthefwmlnkrrtyrsakralfilgpnpls	120
Qy	121	LMTRISVHSVFSMFICTVIINCMFWANSMERSFDMIDPEYVPIGYIYLEAVIKILARGF	180
Db	121	lmtrisvhsvsmfiictviincmfmansemersfmdipeyvfgyiyleavikilargf	180
Qy	181	IVDEFSFLRDPWNWLDPIVGTAIATCFPGSQVNLXSALRTRFRVRKALKAISVTSGLUKIV	240
Db	181	ivdefslrpdwnwldpivgtataicfpgsqvnlsaltrfrvrkalkaisvlsglkiv	240
Qy	241	GALLRSYKKLVDMVWMLTFLCLSFALVGQOLFMIILNOKCIKNCNPNASNKDCFEKER	300
Db	241	gallrsykvldmvwmltflclsifalvgqlfmiilnqckikncnpgnasnkdcfekek	300
Qy	301	DSEDFIMCGTWLGRSPCNGSTCDKTTLPNDNNYTKFDNFGWSFLAMFRVMTQDSMERLY	360
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Qy	361	ROILRTSGIYVFFVFFVIFLGSFYLLNLTLAVVTMAYEEQNRRNVAATEAKEMFQEAQ	420
Db	361	rqlrtsgiyvffvffviflgsfyllnltlavvtmayeeqnrnvaateakekmfqaq	420
Qy	421	QLLREEKEALVANGIDRSSUNLSIQASSFSPPKKRFFGSKTRKSFPMWRGSKTQAASDSE	480
Db	421	qllrееkealvangidrsslnsiqassfsppkkrfgsktrksfpmrgsktaqasadsе	480
Qy	481	DDASKNPQLLEQTKRLSQNLPVDLFDEHVDPLHRQRALSNAVSILTTITIOEQEKFQPCPP	540
Db	481	ddasknpqlleqtkrlsqnlpvdlfdehvdplhrqralnavsiltitmqeqekfqpcfp	540
Qy	541	CGKNLASKYLWDCSPQWLICIKKVLRTIMTDPTELAITICIINVFVLAVEHHNNDDNL	600
Db	541	cgknlaskylwdcspqwlckkvlrtimcdpftelaiticiiinvcflavehnnmdnl	600
Qy	601	KTILKIGNWVFTGFTIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSDDNN	660
Db	601	ktilkignwvftgftiaemclkiialdpvyhfrhgnvfdsisvallsldvlyntlsdnn	660
Qy	661	RSFLASLURVLVPFKLAKSWPTNLTKIIGHSVGALGNLTVLTVTVVIFSVVGMRLFGT	720
Db	661	rsflaslrvlpfkakswptnltkighsvgalgnltvltvvlvfvvvgmrlfgt	720

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RESULT 4
AAB20122
ID AAB20122 standard; Protein; 1765 AA.
XX
AC AAB20122;
XX
XX 30-APR-2001 (first entry)
XX
XX Rat sodium channel NaN.
XX
XX Sodium channel; NaN; rat; tetrodotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
KW diagnosis.
XX
XX
FH Key Location/Qualifiers
FT Domain 125..148
FT /note= "transmembrane domain DI-S1"
FT Domain 157..177
FT /note= "transmembrane domain DI-S2"
FT Domain 191..210
FT /note= "transmembrane domain DI-S3"
FT Domain 216..237
FT /note= "transmembrane domain DI-S4"
FT Domain 254..273
FT /note= "transmembrane domain DI-S5"
FT Domain 338..350
FT /note= "transmembrane domain DI-SS1"
FT Domain 353..358
FT /note= "transmembrane domain DI-SS2, includes Ser
FT residue at position 355 implicated in
FT tetrodotoxin resistance"
FT
FT 371..398
FT /note= "transmembrane domain DI-SS3"
FT Domain 567..591
FT /note= "transmembrane domain DII-S1"
FT Domain 603..624
FT /note= "transmembrane domain DII-S2"
FT Domain 633..654
FT /note= "transmembrane domain DII-S3"
FT Domain 663..682
FT /note= "transmembrane domain DII-S4"
FT Domain 699..719
FT /note= "transmembrane domain DII-S5"
FT Domain 741..750
FT /note= "transmembrane domain DII-SS1"
FT Domain 755..759
FT /note= "transmembrane domain DII-SS2"
FT Domain 774..800
FT /note= "transmembrane domain DII-S6"
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FT /note= "transmembrane domain DIII-S1"
FT Domain 1067..1192
FT /note= "transmembrane domain DIII-S2"
FT Domain 1198..1116
FT /note= "transmembrane domain DIII-S3"
FT Domain 1119..1140
FT /note= "transmembrane domain DIII-S4"
FT Domain 1159..1180
FT /note= "transmembrane domain DIII-S5"
FT Domain 1223..1232
FT /note= "transmembrane domain DIII-SS1"
FT Domain 1236..1241
FT /note= "transmembrane domain DIII-SS1"
FT Domain 1263..1288
FT /note= "transmembrane domain DIII-S6"
FT Domain 1341..1356
FT /note= "transmembrane domain DIV-S1"
FT Domain 1440..1463
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FT Domain 1479..1501
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FT 1513..1527

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FT /note= "transmembrane domain DIV-SS1"
FT 1529..1534
FT /note= "transmembrane domain DIV-SS2"
FT 1558..1584
FT /note= "transmembrane domain DIV-S6"
XX
XX Rattus norvegicus.
OS
XX WO200105831-A1.
PN
XX 25-JAN-2001.
PD
XX 14-JUL-2000; 2000WO-USI9342.
FF
XX 16-JUL-1999; 99US-0354147.
DR
XX (UYYA ) UNIV YALE.
PA
XX Dib-Hajj S, Waxman SG;
XX
XX WPI: 2001-103147/11.
DR N-PSDB; AAF30102.
XX
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium
PT channels, useful for preventing, diagnosing and treating pain,
PT paraesthesia and/or hyperexcitability phenomena.
PT
XX Example 2; Fig 3; 162pp; English.
XX
XX The present sequence is that of novel rat tetrodotoxin resistant
CC sodium channel NaN, as deduced from cDNA (see AAF30102) isolated
CC from a rat dorsal root ganglia tissue library. The sequence
CC shows 69% similarity to human NaN (see AAB20121). NaN belongs to
CC the a-subunit voltage-gated sodium channel protein family. It
CC produces a TTX-R sodium current. Such channels underlie the
CC generation and propagation of impulses in excitable cells such as
CC neurons and muscle fibres. Preferential expression of NaN on
CC sensory neurons innervating the body (dorsal root ganglia) and
CC the face (trigeminal ganglia), but not on other neurons, makes
CC it a very useful target for diagnostic and/or therapeutic uses in
CC relation to acute and/or chronic pain pathologies. A claimed
CC method of treating pain, paraesthesia and/or hyperexcitability
CC phenomena in a human or animal subject involves administering an
CC agent that alters sodium current flow through NaN channels, or
CC which modulates transcription or translation of NaN mRNA, in
CC dorsal root ganglia or trigeminal neurons. NaN polypeptides can
CC be obtained by recombinant expression, and used to treat disorders
CC associated with decreased sodium channel expression, to screen for
CC compounds that modulate sodium channel expression or activity,
CC and to raise antibodies useful as diagnostic agents.
XX
XX Sequence 1765 AA;
SQ

```

```

Query Match 99.7%; Score 9149; DB 22; Length 1765;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1759; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEERYYPVIFPDENFRPFTSDSLAAIKKRIATOKERKKSKDAAEPPQRPQLDKASR 60
Lb 1 meeryypvifpdernfrpftsdslaalekrlaiqkerkkskdaaepprpqldkars 60
Qy 61 KLPKLYGDIPELVTKPLELDLPYKDKHTFMVNLKRRKTIYRFSAKRALFILGFPNPLRS 120
Lb 61 klpklygdippelvtkpleldlpkydkhtfmvlnkkrtiyrfsakralfilgfpnplrs 120
Qy 121 LMIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFICIVILEAVIKLARGF 180
Lb 121 lmirisvhsvfsmfiictviinmcmfmanmsmersfdndipeyvfigiyleaviklrgf 180
Qy 181 IVDEFSFLRDPWNWLDIFIVIGTAITATCPGSQLNSALRTRFVRFAKKAISVIGLKIV 240
Lb 181 ivdefsfldrpdwnwldfivigtaitatcpgsqvnlsalrtfrvralkaisvisgkiv 240

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QY 241 GALLRSYKVLVDVWMLTFLCLISFALYGOQLFMGILNOKICKHNCGPNPASNKDCFEKEK 300
DB 241 gallrsykvkvlvdvwmvltlflclsifalvgqqlfmgilnqkckhncgpnasnkdcfekek 300
QY 301 DSEDFMCGTWLGRPCPNSTCDKTTLPNDNNYTKEDNFGWSFLAPRWVTQDSWERLY 360
DB 301 dsedfmncgtwlgprcpnstcdkttlnpdnnnytkednfgwsflamfrvmtqdsweyly 360
QY 361 RQILRTSGIYVFVFVFFVFLSGSYLENLTAVVTMAYEONRNVAATEAKEKMFQEAQ 420
DB 361 rqiilrtsgiyvfvfvffvflsgsylenltavvtmayeoonrnvaateakekmfqeaq 420
QY 421 QLLREKEALVAMGIDRSSUNLSQASSFSPPKRRKFFSGTRKSPFMRGSKTAQASADSE 480
DB 421 qlireekealvamgidrssunlsqassfsppkrrkffsgtrkspfmrsgsktaqasads 480
QY 481 DDASKNPQLLEOTKRLSONLPVDLFDEHVDPLHRQALSAVSILTIITIOGEKEFOEPCFP 540
DB 481 ddasknpqlleotkrlsqnlpvdlfdehvdplhrqalsavsilittioqekefoepcfp 540
QY 541 CGKNLASKYLWDCSPQWLCKIKKVLRTIMTDPFTELATITICIIINTVFLAVEHHNMDDNL 600
DB 541 cgknlaskylwdcspqwlckikvltimtdpftelaititiciintvflavehnmddnl 600
QY 601 KTLKIGNWVFTGIFIAEMCLKIIFALDPYHYFRHGNVFDISIVALLSLADLYNTLSNN 660
DB 601 ktlkignwvftgifaemclkiialdpynhyfrhgnvfdisaivallsadlyntlsdn 660
QY 661 RSFLASRLVRFKLSKSWPTLNTLIKIIGHSVGCALGNLTWLTIVVIFSVGMRLEGT 720
DB 661 rsflasrlvrfklskswptlntlikiighsvgalnltwltivvifsvvgmrlegt 720
QY 721 KFNKTATVATPRRRHMDNFYHSFLVPRILCGEMTENNMGCMQMDGSPLCIIVFVL 780
DB 721 kfnktatvqprrrhmdnfysflvprilcgemtennmgcmqmdgspclciivfl 780
QY 781 IMVIGKLVNLFIALLNSFSNEEKDGLSEGETRKKVQLALDRFRRAFSFMLHALQSF 840
DB 781 imvigklvnlfiallnsfsneekdglsegetrkkvqlaldrfratsfmlhalqsf 840
QY 841 CCKKCRKNPKPKETTESFAGENKDSILPDARPKWEYDMDALYTGQAGAPLAPAEVE 900
DB 841 cckkcrknspkpkettesfagenkdsilpdarpkweydtmdalytgagaplapaeve 900
QY 901 DDVEYCGEGGALPTSHSAGVQAGDLPPETKOLTSPPDDGVMEVFSEEDLHLSIQSPRK 960
DB 901 ddveycgeggalptshsagvqagdlppetkqlcspddgvmevfseedlhlsiqsprk 960
QY 961 KSDAVSMLSECTIDLANDIFRNLOKTVSPKKQDPDRCPKGLSCHFLCHKTKDRKSPWVLW 1020
DB 961 ksdavsmsectidlandifrnloktvspkkqdpdrckpqlschflchktdkrkspwvlw 1020
QY 1021 WNIKRTQYIVKHSWFSEFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCRTDNTFTIFL 1080
DB 1021 wnirktyqivkhswfesfiifvillssgalifedvnlpsrpqveklrcrtdntftifl 1080
QY 1081 LEMILKVVAGCFRBYFTSANCWLDLIVVYSVLSLMLNPLSKSRFTLRALPLALSOFE 1140
DB 1081 lemilkvvagcfryftsancwldlilvvysvlsmlnplsksrftlralsqfe 1140
QY 1141 GMKVYVALISAIPAILNLVLVCLIFWLVCILGNVLFSGKFGRCINGTDINMYLDTEV 1200
DB 1141 gmkvvyvalisaipailnlvlvclifwlvclivgnlvfsgkfgrcingtdinmyldtev 1200
QY 1201 PNRSQCNISNYSWKVPQVFNQVNGVAYLALLQVATYKGLWEIMNAAVDSREKDEQDFEA 1260
DB 1201 pnrscqcnisnyswkvpqvnqvnaylallqvatykgwleimnaavdsrekdeqdf 1260
QY 1261 NLXAYLFFVVFIFGSEFTLNLFTGVIIIDNPNQOQKLGQDIFMTSEQKYYNAMKKLG 1320
DB 1261 nlxaylffvfvfifgseftlnlftgviiidnfnqgqkllg9gdfimteeqkyynamkklg 1320

RESULT 5

AAB20123 standard; Protein; 1765 AA.

ID AAB20123;

AC AAB20123;

DT 30-APR-2001 (first entry)

DE Rat sodium channel NaN.

KW Sodium channel; NaN; rat; tetrodotoxin resistant; pain;
paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
diagnosis.

FH Key Location/Qualifiers

FT Domain 125..148

FT /note= "transmembrane domain DI-S1"

FT Domain 157..177

FT /note= "transmembrane domain DI-S2"

FT Domain 191..210

FT /note= "transmembrane domain DI-S3"

FT Domain 216..237

FT /note= "transmembrane domain DI-S4"

FT Domain 254..273

FT /note= "transmembrane domain DI-S5"

FT Domain 338..350

FT /note= "transmembrane domain DI-Ss1"

FT Domain 353..358

FT /note= "transmembrane domain DI-Ss2, includes Ser
residue at position 355 implicated in
tetrodotoxin resistance"

FT Domain 371..398

FT /note= "transmembrane domain DI-Ss3"

FT Domain 567..591

FT /note= "transmembrane domain DII-S1"

FT Domain 603..624

FT /note= "transmembrane domain DII-S2"

FT Domain 633..654

FT /note= "transmembrane domain DII-S3"

FT Domain 663..682

FT Domain /note= "transmembrane domain DII-S4"
 FT 699..719
 FT /note= "transmembrane domain DII-S5"
 FT 741..750
 FT /note= "transmembrane domain DII-SS1"
 FT 755..759
 FT /note= "transmembrane domain DII-SS2"
 FT 774..800
 FT /note= "transmembrane domain DII-S6"
 FT 1029..1052
 FT /note= "transmembrane domain DIII-S1"
 FT 1067..1192
 FT /note= "transmembrane domain DIII-S2"
 FT 1198..1116
 FT /note= "transmembrane domain DIII-S3"
 FT 1119..1140
 FT /note= "transmembrane domain DIII-S4"
 FT 1159..1180
 FT /note= "transmembrane domain DIII-S5"
 FT 1223..1232
 FT /note= "transmembrane domain DIII-SS1"
 FT 1236..1241
 FT /note= "transmembrane domain DIII-SS1"
 FT 1263..1288
 FT /note= "transmembrane domain DIII-S6"
 FT 1341..1356
 FT /note= "transmembrane domain DIV-S1"
 FT 1440..1463
 FT /note= "transmembrane domain DIV-S4"
 FT 1479..1501
 FT /note= "transmembrane domain DIV-S5"
 FT 1513..1527
 FT /note= "transmembrane domain DIV-SS1"
 FT 1529..1534
 FT /note= "transmembrane domain DIV-SS2"
 FT 1538..1584
 FT /note= "transmembrane domain DIV-S6"
 FT Misc-difference 652 /note= "encoded by CTN"
 FT Misc-difference 1334 /note= "encoded by AAN"
 FT

XX Rattus norvegicus.

OS WO200105831-A1.

XX 25-JAN-2001.

XX 14-JUL-2000; 2000WO-US19342.

XX 16-JUL-1999; 99US-0354147.

XX (UYIA) UNIV YALE.

XX Dib-Hajj S, Waxman SG;

XX WPI; 2001-103147/11.

XX N-PSDB; AAF30102.

XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -

XX Example 2; Page 98-103; 162pp; English.

XX The present sequence is that of novel rat tetrodotoxin resistant sodium channel Nan, as deduced from cDNA (see AAF30102) isolated from a rat dorsal root ganglia tissue library. The sequence shows 69% similarity to human Nan (see AAB20121). Nan belongs to the a-subunit voltage-gated sodium channel protein family. It produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of Nan on

CC sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through Na^v channels, or which modulates transcription or translation of Na^v mRNA, in dorsal root ganglia or trigeminal neurons. Na^v polypeptides can be obtained by recombinant expression, and used to treat disorders associated with decreased sodium channel expression, to screen for compounds that modulate sodium channel expression or activity, and to raise antibodies useful as diagnostic agents.

XX Sequence 1765 AA;

Query Match 99.7%; Score 9141; DB 22; Length 1765;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1758; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEERYYPVIFPDERNFRPFTSDSLAAIKKRIATOKERKKDKAAAEPPRPQDLKASR 60
 Dd |||||
 Qy 1 MEERYYPVIFPDERNFRPFTSDSLAAIKKRIATOKERKKDKAAAEPPRPQDLKASR 60
 Dd |||||
 Qy 61 KLPKLYGDIPPELVTKPLEDLDPYKDKHTPMVLNKKRTIYRFSAKRALFTLGPFPNPLRS 120
 Dd |||||
 Qy 61 KLPKLYGDIPPELVTKPLEDLDPYKDKHTPMVLNKKRTIYRFSAKRALFTLGPFPNPLRS 120
 Dd |||||
 Qy 121 LMIRISVHSVSMFIICITVIINCMFMANSMERSFDNDIPEYVFIIGIYILEAVIKILARGF 180
 Dd |||||
 Qy 121 LMIRISVHSVSMFIICITVIINCMFMANSMERSFDNDIPEYVFIIGIYILEAVIKILARGF 180
 Dd |||||
 Qy 181 IVDEFSLRDPWNWLDFTIVIGTAITATCPGQVNLALTRFRVFRALKAKISVIGLKVIV 240
 Dd |||||
 Qy 181 IVDEFSLRDPWNWLDFTIVIGTAITATCPGQVNLALTRFRVFRALKAKISVIGLKVIV 240
 Dd |||||
 Qy 241 GALLRSVKKLVDMVLTLCISIFALVGQQLFMGLNCKIKHNGPNPASKDKCFEKEK 300
 Dd |||||
 Qy 241 GALLRSVKKLVDMVLTLCISIFALVGQQLFMGLNCKIKHNGPNPASKDKCFEKEK 300
 Dd |||||
 Qy 301 DSEDFIMCGTWLGSRPCNGSTCDKTTLPNDNNYTKFDNFGWSFLAMPRVMTQDSWERLY 360
 Dd |||||
 Qy 301 DSEDFIMCGTWLGSRPCNGSTCDKTTLPNDNNYTKFDNFGWSFLAMPRVMTQDSWERLY 360
 Dd |||||
 Qy 361 RQILRTSGIYFFVFFVVFILGSPYLLNLTAVVTMAYEONRNVAATEKAKMFQQAQ 420
 Dd |||||
 Qy 361 RQILRTSGIYFFVFFVVFILGSPYLLNLTAVVTMAYEONRNVAATEKAKMFQQAQ 420
 Dd |||||
 Qy 421 QLLREKEALVAMGIDRSSLNSLOASSPSPKPKRFFGSKTRKSPFMGRSKTAQASADSE 480
 Dd |||||
 Qy 421 QLLREKEALVAMGIDRSSLNSLOASSPSPKPKRFFGSKTRKSPFMGRSKTAQASADSE 480
 Dd |||||
 Qy 481 DDASKNPQLLEQTKRLSONLPVDLFDEHVDPLHRQALSAVSILTTITQEQEKFCPCFP 540
 Dd |||||
 Qy 481 DDASKNPQLLEQTKRLSONLPVDLFDEHVDPLHRQALSAVSILTTITQEQEKFCPCFP 540
 Dd |||||
 Qy 541 CGKNLASKYLVWDCSPQWLCKIKKVLRTIMTDPFFTELATITICIIINTVFLAVEHHMDDNL 600
 Dd |||||
 Qy 541 CGKNLASKYLVWDCSPQWLCKIKKVLRTIMTDPFFTELATITICIIINTVFLAVEHHMDDNL 600
 Dd |||||
 Qy 601 KTIKIGNWVPTGIFIAEMCKLIITADPYHYFRHGNVDFDSIVALLSLADLYNTLSNN 660
 Dd |||||
 Qy 601 KTIKIGNWVPTGIFIAEMCKLIITADPYHYFRHGNVDFDSIVALLSLADLYNTLSNN 660
 Dd |||||
 Qy 661 RSFIASLRVLRVFKLAKSWPTLNTLIKTIHSGVAGLNLTVLTIWVIFSVGMRLFGT 720
 Dd |||||
 Qy 661 RSFIASLRVLRVFKLAKSWPTLNTLIKTIHSGVAGLNLTVLTIWVIFSVGMRLFGT 720
 Dd |||||
 Qy 721 KFNKTATATQPRRRHMDNFYSLVFWFRILGGEWIENWGMQMDGSGPLCTIIVFL 780
 Dd |||||
 Qy 721 KFNKTATATQPRRRHMDNFYSLVFWFRILGGEWIENWGMQMDGSGPLCTIIVFL 780
 Dd |||||

Qy 781 IMVIGKLVNLFTALLNSFNEEKDGLSEGETRKTQVQALDRFRRAFSFMLHALQSF 840
Db 781 imvigklvnlftallnlsfneekdglsegetrktqvqaldrfrfrafsmhalqsf 840
Qy 841 CCKCRRKNSPKKETTETESFAGENKDSLLDPARPKWKEVDTDMALYTQAGAPLAPAEVE 900
Db 841 cckcrrknsppkettetefagenkdsllparpkeytdmalytgagaplapaeve 900
Qy 901 DDVEYCEGGALPTSOHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRK 960
Db 901 ddveyceggalptsohsagvqagdlppetkqltspddqgvemevfseedhlhlsiqsprk 960
Qy 961 KSDAVSMLSEGSTIDLNDIFRNALQTVSPKQDPKRCFPKGLSCHFLCHTKDKRKSPWYLV 1020
Db 961 ksdavsmlsegstidlndifrnalqtvspkqdpkrcfpkglfchtkdkrksppwlv 1020
Qy 1021 WNIKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPOVEKLLRCRDNFTFTFL 1080
Db 1021 wnirktcyqivkhswfesfiifvillssgalifedvnlpsrpovekllrcrctdniftftfl 1080
Qy 1081 LEMILKWVAFGRFRYFTSAWCWDLFIIVVSVLSLMLNPLSKSPRTLRLALPLRLALSQFE 1140
Db 1081 lemilkwvafgrfryftsaawcwlfiivvsvlsmlnplsksftrtlalplrlalsqfe 1140
Qy 1141 GMKVYVALISAIPAILNVLVCLFIWLVFCILGVNLFSGRGCINGTIDINMYLDFTEV 1200
Db 1141 gmkvvyvalisaipailnvlvclfiwlvfcilgvnlfsgrgfcngtldinmyldftev 1200
Qy 1201 PNRSGNISYVSWKVPQVNFQNGNAYLALQVATYKGLWEIMNAVDSREKDSQDPPEA 1260
Db 1201 pnrsgnisyvswkvpqvnfnvngnaylaliqvatykgwleimnaavdsrekdeqdpfea 1260
Qy 1261 NLYAYLVFVPTIFGSRFTLLFTGVITDNEQOQKLGIGDIFWTEQKYYNAMKKLG 1320
Db 1261 nlyaylvfvptifgsrftllftgvitdneqoqkllgigdifwteqkyynamkkllg 1320
Qy 1321 TKKQKPIRPLNCKQAFVFLVTSQVFDVIIIGLIVLNMIMMAESADQPKDKVKKTPDI 1380
Db 1321 tkkqkpiplrnlncqafvflvtsqvfdiviilglivlnmimmaesadqpkdkvkktpdi 1380
Qy 1381 LNIAPVIFTTECLIKVPALQKHFTNGWNLFDVWVVLSTIISLVSLESDISFPPTL 1440
Db 1381 lniapviftteclikvpalqkhftngwnlfdcvvvvlsistivslrledsdisfpptl 1440
Qy 1441 FRVRLARIGRILRLVRAARGIRTLPLALMSLPSLFRNIGLLFLVMPFIYALFGMSWFSK 1500
Db 1441 frvrlarigrilrlvraargirtlplalmslpslfrnigllflvmpfiyalfgmswfsk 1500
Qy 1501 VKGSGIDDIIFNETFTGSMCLFQITTSAGWDTLLNPMLEAKHCNSSQDSQQQPIA 1560
Db 1501 vkgsgiddifnetftgsmclfqittsagwdtllnplmleakehcnssqdsccqppia 1560
Qy 1561 VYFVSYIIISFLIVNMVYIAVILENFNTATESEDPDGDDFEIFYEVWEKFDPEASQF 1620
Db 1561 vyfvsyiiiisflivnmvyiavilenfntateesedplgdddfeyfeywekfdepeasqf 1620
Qy 1621 IQYSALSDFADALPEPLRVAKPNKFOFLVMDLPVWVGDLRHCMDVLFATFTRVLGDSGL 1680
Db 1621 iqysalsdfadalpeplrvaqpnkfoflvmdlpvmvgdlrhcmdvlfatftrvlgdssgl 1680
Qy 1681 DTMTMEEKPMEANPKKLEPIVITTTKRKEEQGAIVIRAYKKHMKVKKRLKDRS 1740
Db 1681 dtmtmeekpmeanpkklepivitttkrkeeqgaaviraykkmkvkrlkdrs 1740
Qy 1741 SSSHQVFCNGDLSLDVAKVVKHND 1765
Db 1741 ssshqvfcngdlsldvakvkvhnd 1765

RESULT 6

AAY06597

ID AAY06597 standard; Protein; 1765 AA.

XX

AC AAY06597;
XX 26-OCT-1999 (first entry)
XX Mouse sodium channel NaN.
XX NaN; sodium channel; ion transport; mouse; dorsal root ganglia;
XX pain; paraesthesia; hyperexcitability; therapy.
XX Mus musculus.
XX
FH Key Location/Qualifiers
FH Region 125..148
FH /label= DI-S1
FH /note= "domain I transmembrane segment S1"
FH Region 159..179
FH /label= DI-S2
FH /note= "domain I transmembrane segment S2"
FH Region 193..213
FH /label= DI-S3
FH /note= "domain I transmembrane segment S3"
FH Region 219..240
FH /label= DI-S4
FH /note= "domain I transmembrane segment S4"
FH Region 257..276
FH /label= DI-S5
FH /note= "domain I transmembrane segment S5"
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FH /label= DI-SS1
FH /note= "domain I transmembrane segment SS1"
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FH /label= DI-SS2
FH Region 374..401
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FH /note= "domain II transmembrane segment S2"
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FH /note= "domain II transmembrane segment S3"
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FH Region 775..800
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FH Region 1099..1117
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1558..1584
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/note= "domain IV transmembrane segment S6"

W09938889-A2.

05-AUG-1999.

29-JAN-1999; 99WO-US02008.

20-NOV-1998; 98US-0109402.

29-JAN-1998; 98US-0072990.

(UYUA) UNIV YALE.

Dib-Hajj S, Waxman S;

WPI; 1999-479168/40.
N-PSDB; AAX87601.

New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability phenomena

Claim 1; Fig 7B1-2; 91pp; English.

This is the predicted amino acid sequence of the mouse Na^v channel, as deduced from isolated mouse Na^v cDNA (see AAX87601). Na^v is a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. Rat, mouse and human Na^v nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express Na^v, methods for identifying agents that modulate Na^v channel activity or Na^v channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, anaesthesia and hyperexcitability phenomena. The preferential expression of Na^v in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord.

Db 959 arksdaaslsestidlnidfrlqktvspqkqrcfpkglscifloctikkspw 1018
QY 1018 VLWNIRKTCQIVKHSWFESIFIEVILLSSGALIFEDVNLPSRQVEKLLRCTDNIETFE 1077
Db 1019 vlwnlktcyqivkhswfesifivllssgalifedvnlpsrpqveklkcdnlf 1078
QY 1078 IFLEMLIKWAFGRFRYFTSAMCWLDFLIVVSVLSMLNPSIKSFRTLRALPLRLALS 1137
Db 1079 iflemlilkwafgrkyftsawcwlflivvsvlsnltnlpslksfrnlralplrlals 1138
QY 1138 QFEGMKVVVALISAIPAILNVLVCLIFWLVCILGVNLPSGKFGRCINGTDINMYLDF 1197
Db 1139 qfegmkvvvalmsaipailnvlvclifwlvcilgvnlpsgkfgrcingtdinkyna 1198
QY 1198 TEVNRQOCISNYSWKVPOVFNQGNAYLALLOVATYKGLWLEIMNAAYDSREKDEQPD 1257
Db 1199 snvpnqgcqvsnvtykvpvnnfdvngnaylallqvetykgwidmnaavdsrgkdeqpa 1258
QY 1258 FEANLYAYLVFVFIIFGSPFTLNLFITGVINDPNQOQKLGQDIFMTEEQKYYNAMK 1317
Db 1259 feanlyaylvfviifgspftlnlfvgviidnfnqgkklgqgdi fnteeqkyynamk 1318
QY 1318 KLCTKKPKQPIPRPLNKQAFVFDLVTQSOFDVIILGLIVLNMIIIMMAESADQPKVKKT 1377
Db 1319 klgtkpkpkiprplnkqafvdlvtqsqfvdvliqlivtnmliimmaesegqpnevkki 1378
QY 1378 FDIINAFVVFTECLIKVPALROHYFTNGWNLFCVWVVSLSIISLVSRLESDISFP 1437
Db 1379 fdiinavfviftveclikvfaqrhyftngwnlfdcvvvvlsistlvsglensnv-fp 1437
QY 1438 PTLFRVVRRLARIGRILRLVRAARGIRTLFALMMSLPSLFNIGLGLFLVMFIYAIFQMSW 1497
Db 1438 ptlfrvrlarigrilrlvraargirtlflalmmslpslfnigllflvmfiyaifqmsw 1497
QY 1498 FSKVKKSGDDIDFNFETFTGSMCLFQITTSAGWDFTLLNPMLEAKEHCNSSQDSQQP 1557
Db 1498 fskvkrgsgddidnfdtfgsmclcfqittsagwdallnplmieskascnssqscqqp 1557
QY 1558 QIAVYVSVYIIISFLIVWNNYIAVILENFNTAPEESEDPLGEDDFEIFYEVWEKFPDEA 1617
Db 1558 qiaivvsvyisflivwvnyiavilennfntateesedplgeddfefiyeiwekfdepa 1617
QY 1618 SQTQYSALSDFADALPEPIRVAKPNKFQFLVMDLPMVMDRCHMDVLFATFTRVLGDS 1677
Db 1618 tqfiqyslsdadalpepirvakpnr-fqflmldpvmgdrhlcmvdlfafttrvlgn 1677
QY 1678 SGLDTMTMEERPMANPEKLYEPIVTTTKREEQGAAYIQRAYRKHEKWKVLRK 1737
Db 1678 sgldtmtmeekfmeanpklyepivtttkreeeqgaayiqrayrkhmekwmiklkl 1737
QY 1738 DRSSSHQVFCNGDLSSLDVAKVKVHND 1765
Db 1738 grssslqvfcngdlsldvapkikhvd 1765

RESULT 7

AAB20124
ID AAB20124 standard; Protein; 1765 AA.
XX AC AAB20124;
XX DT 30-APR-2001 (first entry)
XX DE Mouse sodium channel Nan.
XX KW Sodium channel; NaN; rat; tetrodotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
KW diagnosis.
XX PH Key Location/Qualifiers
XX FT Domain 125..148
/note= "transmembrane domain DI-S1"

Domain 159..179
/note= "transmembrane domain DI-S2"
Domain 193..212
/note= "transmembrane domain DI-S3"
Domain 219..240
/note= "transmembrane domain DI-S4"
Domain 257..276
/note= "transmembrane domain DI-S5"
Domain 342..361
/note= "transmembrane domain DI-SS1"
Domain 356..361
/note= "transmembrane domain DI-SS2"
Domain 374..401
/note= "transmembrane domain DI-S6"
Domain 569..594
/note= "transmembrane domain DII-S1"
Domain 606..629
/note= "transmembrane domain DII-S2"
Domain 636..644
/note= "transmembrane domain DII-S3"
Domain 665..684
/note= "transmembrane domain DII-S4"
Domain 701..720
/note= "transmembrane domain DII-S5"
Domain 743..751
/note= "transmembrane domain DII-SS1"
Domain 756..760
/note= "transmembrane domain DII-SS2"
Domain 775..800
/note= "transmembrane domain DII-S6"
Domain 1031..1053
/note= "transmembrane domain DIII-S1"
Domain 1068..1193
/note= "transmembrane domain DIII-S2"
Domain 1199..1117
/note= "transmembrane domain DIII-S3"
Domain 1121..1140
/note= "transmembrane domain DIII-S4"
Domain 1160..1180
/note= "transmembrane domain DIII-S5"
Domain 1225..1233
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Domain 1237..1242
/note= "transmembrane domain DIII-SS1"
Domain 1264..1289
/note= "transmembrane domain DIII-S6"
Domain 1343..1356
/note= "transmembrane domain DIV-S1"
Domain 1381..1401
/note= "transmembrane domain DIV-S2"
Domain 1408..1430
/note= "transmembrane domain DIV-S3"
Domain 1339..1463
/note= "transmembrane domain DIV-S4"
Domain 1479..1499
/note= "transmembrane domain DIV-S5"
Domain 1513..1527
/note= "transmembrane domain DIV-SS1"
Domain 1529..1534
/note= "transmembrane domain DIV-SS2"
Domain 1558..1584
/note= "transmembrane domain DIV-S6"
Mus musculus.
OS WO200105831-A1.
PN 25-JAN-2001.
XX PD 14-JUL-2000; 2000WO-US19342.
XX PF 16-JUL-1999; 99US-0354147.
XX PR XX

PA (UYAA) UNIV YALE.
 XX D1b-Hajj S, Waxman SG;
 XX WPI; 2001-103147/11.
 DR N-PSDB; AAF30103.
 XX
 XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium
 PT channels, useful for preventing, diagnosing and treating pain,
 PT paraesthesia and/or hyperexcitability phenomena -
 XX Example 3; Fig 7B; 162pp; English.
 XX
 CC The present sequence is that of novel mouse tetrodotoxin resistant
 CC sodium channel Nan, as deduced from the Scn11a gene (see AAF30103)
 CC isolated from a mouse trigeminal ganglia cDNA. The sequence shows
 CC 68% similarity to human Nan (see AAB20121). Nan belongs to the
 CC a-subunit voltage-gated sodium channel protein family. It produces
 CC a TTX-R sodium current. Such channels underlie the generation and
 CC propagation of impulses in excitable cells such as neurons and
 CC muscle fibres. Preferential expression of Nan on sensory neurons
 CC innervating the body (dorsal root ganglia) and the face (trigeminal
 CC ganglia), but not on other neurons, makes it a very useful target
 CC for diagnostic and/or therapeutic uses in relation to acute and/or
 CC chronic pain pathologies. A claimed method of treating pain,
 CC paraesthesia and/or hyperexcitability phenomena in a human or
 CC animal subject involves administering an agent that alters sodium
 CC current flow through Nan channels, or which modulates transcription
 CC or translation of Nan mRNA, in dorsal root ganglia or trigeminal
 CC neurons. Nan polypeptides can be obtained by recombinant
 CC expression, and used to treat disorders associated with decreased
 CC sodium channel expression, to screen for compounds that modulate
 CC sodium channel expression or activity, and to raise antibodies
 CC useful as diagnostic agents.
 XX
 SQ Sequence 1765 AA:
 Query Match 88.9%; Score 8153; DB 22; Length 1765;
 Best Local Similarity 88.7%; Pred. No. 0;
 Matches 1569; Conservative 94; Mismatches 99; Indels 6; Gaps 5;
 QY 1 MEERYYPVPPDERNRPFTSDSLAAIKKRTAIQKERRKSKDKAAAPQRPOLDKASR 60
 DB 1 meeryypvfpdenrpfdfdsllaekritiquekkskdaatepqrpqldklsr 60
 QY 61 KLPLKXGDIPELVTKPLEDLPYKDKHTFMWLNKRTIYRSAKRALFILGPNPLRS 120
 DB 61 klplklygdvppdliakpliedldpfykdhtfmvlnkrtiyrfsakralfilgpnplrs 120
 QY 121 LMIRISVHSVSMFIICVTIINCFMAN--SMERSFNDPIPEYVFIGIYLEAVIKILAR 178
 DB 121 fmirisvhsvsmfiicvtiincmfmanssvdsrpsnipeyvfilygleavikilar 180
 QY 179 GFIVDEFSLRDPNNWLDIVIGTAIATCPGSOV--NLSALRTPRFRALKATISVIGLKL 237
 DB 181 gflvdefsyrdpwnwldivigtaiapcflgnkvnnlstlrfrvralkaisvisgkl 240
 QY 238 VIVGALLRSVKLVDMVNLFLCLISIFALVGOQLFMGLNOKCIKHNCGNPNASNKDCFE 297
 DB 241 vivgallrsvklvdmvnlflclsifalvgqqlfmgilsgkclkdcdgpnafsnkdcfv 300
 QY 298 KENDSEDFIMCGTWLGRPCNGSTCDKTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWE 357
 DB 301 kendsedfimcgnwlgrrscpdgstcnktfnpdnytnfdstfgwsflamfrvmtqdswe 360
 QY 358 RLYRQILRTSGIVFVFVFFVIFLGSFYLLNLTAVVTMAYEONRNVAATEAKEMFQ 417
 DB 361 klyrqilrtsgyifvfvffviflgsfyllnltlavvtmayeeqnrnvaateakemf 420
 QY 418 EAQOLLREKEALVAMGIDRSSLSNLSOASSFSKKRFFGSKTRKSFPMRSGKTAQASAS 477
 DB 421 eaqllreekealvamgidrtsslnslqassfsppkrrffgsktrksfpmrsgsktaras 480
 QY 478 DSEDDASKNPOLLBQTKRLSONLPVDLDFDEHVDPLHRORALSAVSILTIITIQEKEQEP 537
 DB 481 dseddasknpqlleqtkrlsqnlpvelfdenvdpbhrqalsavsiltitmeqekseqep 540
 QY 538 CFCGKNLASKYLWDCSPQWLCKIKVLRITMTDPFTTALAITICITINTVFLAVEHHNMD 597
 DB 541 cfcgknlaskeylvwecspwlcikvltqtmtdpftelaiticivntvflamehnmmd 600
 QY 598 DNLTILKIGNWVPTGIFIAEMCLKIIALDPYHYFRHGNVNVFDSIVALLSLADLYLNTLS 657
 DB 601 nslkdilkgwnvftgifaemclkiialdpypfhyfrhgnwifdsivalvsldvlfhkl 660
 QY 658 DNNRPSFLASRLVRFVFLAKSWPPLNTLTIKIHSVGALGNLTVVLIVVIFPSVGMRL 717
 DB 661 -knlsflasrlvrfvflakswptlntliklghsvgalgnltvltivvifsvgmrl 719
 QY 718 FGTFKNATAYATQERRRRWHMDNFYHSFVFRILCGEWENMGCMQMDGSPCLCIIV 777
 DB 720 fgakfntc-stpeslrrwhmgdfyhsflvfrilcgewenmwcemqemegspclviv 778
 QY 778 FVLIMVIGKLVVNLFIALLNFSNEEKDGSLEGETRKTQVQLALDRFRRAFSFMLHAL 837
 DB 779 fvlmvgvklvlnfiallnfsneekdgnpegetrktkvqlaldrfsrafymaral 838
 QY 838 QSFCCCKRRKNSPKPKETTESFAGENKDSILDPARWKEYDDTMALYTGAGAPLAPLA 897
 DB 839 qnfeckrckrrqnsqpkneatesfagesrdatltrskwydsentlytgagaplapla 898
 QY 898 EVEDDVYCEGEGALPTQSHSAGVQAGDLPETKOLTSPODOGVEMEVSEEDLHLSTQS 957
 DB 899 keeddvcegedasptsqseaqcdlplktrlpddhgvemevseeednlhlstqs 958
 QY 958 PRKSDAVSMLSECTIDLNDIFRNLOKTVSPKQPPRCFPKLSCHFLCHKTDRKSPW 1017
 DB 959 arkksdaasmseccstidlnodfrnlqktvspkqpprcfpklschflccktkkkspw 1018
 QY 1018 VLMWNIRKTCQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCDTNTFTF 1077
 DB 1019 vlmwnlrkctqivkhswfesfiifvillssgalifedvnlpsrpqvckllkcdntftf 1078
 QY 1078 IFLEMLILKWAQFGRFRTSACWLDPLVIVSVLSIMNLPKLSFRTLRALPLRLALS 1137
 DB 1079 iflemlilkwafgrfkyftsawcldplvsvlsitnlpnksfmrlnalplrlals 1138
 QY 1138 QFEGMKVYVVALISAIPAILNVLVCLIFWLFCILGVNLFSGKFGRCINGTDINMYLDF 1197
 DB 1139 qfegmkvvyvalmsaipailnvlvclifwlfilgvnffsgkfgrcingtdinkyfna 1198
 QY 1198 TEVPNRSQCNISNYSWKVPQVQVFNEDVGNVAYLALLOVATYKGLWEIMAAVDSREKDEQPD 1257
 DB 1199 snvpngqeqcivsnvtykvpvntfdvgnaylalliqvatykgwldimaaavdsrgkdeqpa 1258
 QY 1258 FEANLYALYFVVFIFRFGSPFTLNLFGVIDNFNOOKKLGODIFMTBEOKKYNNAMK 1317
 DB 1259 feanlyalyfvvfifrgsftlnlfgvidnfnqgqklgqgqifmteeqkkyynamk 1318
 QY 1318 KLGTTPKQKPIPRPLNKCQAFVFDLVTSQVFDVFIILGLIIVLNMIMMAESADQPKVKKT 1377
 DB 1319 klgttkpqpklprplnkcqafvdlvtsqvfdvilglivtnmimaesegqpkvkkk 1378
 QY 1378 FDLINIAFVFTTECLIKVFPALRQHYFTNGWNLFDVGVVVSIIISILVSRLESDSISFP 1437
 DB 1379 fdlinivfvftveclikvfpalrqhyftngwnlfdcvvvvsiisilvsglensv-fp 1437
 QY 1438 PTLFRVRLARIGRILRLVRAARGIRTLFALMMSLPSLFNIGLLLVFMFIYAFGMSW 1497
 DB 1438 ptlfrvrlarigrilrvraargirtllfalmmsslpslfniglllflvmfiyafgmw 1497
 QY 1498 FSKVKGSGIDIDIFNFTFTGSMCLCQITTSAGWDTLLNPMLEAKHCHNCSOSSQSQP 1557
 DB 1498 fskvkrsggididfnftftgsmclcfqittsagwdallnmpleskascnsssqscqp 1557

Qy	1558	QIawvFVSvYIIISfLIVVMVIAVLNFNTATSESDPEIGEDDFETFYVWEKFDPEA	1617
		: : : : : : : : : : :	
Db	1558	qiaIvfvSYIIISfLIVVMVIAVLNFNTATEESDPIGEDDFEIfYEIWKFdPeA	1617
		: : : : : : : : : :	
Qy	1618	SQFTQSALSDFAADALPEPLRVAKPNKQFGLVMDLPVMVGDRGLHCMDVLFAFTTRVLGDS	1677
		: : : : : : : : : : :	
Db	1618	tqfiqyslsdsfadaLpeplrvakpnrtqflmmdlpvmvgdrghcmdivlfafttrvlrgns	1677
		: : : : : : : : : : :	
Qy	1678	SGLDTVKTMMEEKFMENPFFKLYPEPVITVTTKRKEEEOGAAVIORAVRKHKMKVKLRLLK	1737
		: : : : : : : : : :	
Db	1678	sgldtmkammeekfmeeanpfklyepvitttkrkeeeacaaviqrayrrhmekmikiklk	1737
		: : : : : : : : : :	
Qy	1738	DRSSSHQVFCNGDSLSDLVAKVKVHND	1765
		: : : : : : : : : :	
Db	1738	arssslavfcngadlsslsvokikvhcd	1765

RESULT 8

RESOL 0
AAB20121
ID AAB20121 standard; Protein; 1791 AA.

AAC 20121:

DT 30-APR-2001 (first entry)

Human sodium channel Na_v

AA Sodium channel; NaN; human; tetradotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
KW diagnosis.

OS Homo sapiens.

xx PN WO200105831-A1.

25-JAN-2001.

14-JUL-2000: 2000WO-US19342.

PR 16-JUL-1999: 99US-0354147.

PA (UYYA) UNIV YALE.

PI Dib-Hajj S. Waxman SG:

WPI: 2001-103147/11.

DR N-PSDB: AAF30101.

PT Nucleic acid molecules encoding human tetradotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -

PS Claim 7; Fig 11B; 162pp; English.

The present sequence is that of novel human tetrodotoxin resistant sodium channel NAN, as deduced from a cDNA clone (see AAF30101) isolated from human dorsal root ganglia tissue. NAN belongs to the a-subunit, voltage-gated sodium channel protein family. It produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NAN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NAN channels, or which modulates transcription or translation of NAN mRNA, in dorsal root ganglia or trigeminal neurons. NAN polypeptides can be obtained by recombinant expression and used to treat disorders associated with decreased sodium channel expression, to screen for compounds that modulate sodium channel expression or activity, and to raise antibodies useful as diagnostic

QY 929 ETKOLTPDQGVEMVEFSEEDLHLSIOSPRKSDAVSMLESCSTIDNIDFRNLQKTVS 988
 Db 952 enktptsqrvqsveidmfsephltiqdprkksdvtsilsecstidldqdgfwlpemv- 1010
 QY 989 PKQPDRCFFKGLSCHFLCHKTRKSPWLVWNNIRKTCYOIVKHSWFESFIIFVILLSS 1048
 Db 1011 pkqperclpfgccfpccsvdkrkppwlvwnlrkrcyqivkhswfesfiifvillss 1070
 QY 1049 GALLIFEDVNLPSRQVEKLLACTONITFTFLELLEMLKWAFAFGFRFTSACWDLDELIV 1108
 Db 1071 galledvnlkqkqelinctdiifhilemvlkwaafgkyftsawccldfiiv 1130
 QY 1109 VVSLSLMLNPLSLKSFRTLRALRSLSOPEGKMKVVVYALISALPALNLLVCLIFWL 1168
 Db 1131 ivsvttlinmelksftrlralpralsqfegmkvvvnalgaipalnlvclifwl 1190
 QY 1169 VFCILGNVLSFGKRCINGRDINMYLDFTEVPMRSCNITSNYSWKVPQVNFVGNAYL 1228
 Db 1191 vfcilgyvffsgkfgkcingtd--svinytiitnksqcesgnfswinqkvnfdnvgayl 1248
 QY 1229 ALLQVARYKGLWLETMNAVDSREKDEQDPEANLYAYLVFVFIIFSFFTLNLFIGVII 1288
 Db 1249 allqvarkwmdliyaavdstekqepetesnlglyfvvfiifsgfftnlfigvii 1308
 QY 1289 DNFMQOKKLGQDIFMTEQKYYNAMKLGTKPKPIRPLNKCOAFVFDLVTQVF 1348
 Db 1309 dnfmqokk199qdfnteeqkyynamkklgskkpkpripnpinkcqlvfdlvtqsif 1368
 QY 1349 DVILGILVLMITMAESADQPKDKVTKFTDILNTAFVFIPTIECLIKVFAALROHYTNG 1408
 Db 1369 diiisililmismaesynqpkamksildhlnwfvviftleclikifalrpyyftng 1428
 QY 1409 WNLFDVWVLSIISTLVSRLESD--ISFPPTLFRVVRRLARIGRILRLVRAAGIRILLF 1467
 Db 1429 wnlfdvwlsvlsvstmlstlengehipfpptlfrivrlarigrilrvraagirllf 1488
 QY 1468 ALMMSLPLFNIGLLEFLWFIYAFGMWFSKVKKGGIDDIENFETFGSMCLCFQIT 1527
 Db 1489 almslpslfnigllflimfiyalgmwfskvnopesgiddifnftfasmclcfqis 1548
 QY 1528 TSAGWDTLLNPLBAKEHCNSSODSCQOQIAVYVYFVYIIISFLIVNNYIAVILENF 1587
 Db 1549 tsagwdallsplmrksescnss--enchlpgiatyfvsvyiliiisflivnnmyiavilenf 1607
 QY 1588 NTATESEDPGEDDFFETFEVWEKEDPEASQFTQYSALSDFADALPEPLRVAKPNKQF 1647
 Db 1608 ntateesedplgeddfdyevwekfdeacqfkyksalsdfadalpeplrvakpnkyqf 1667
 QY 1648 LVMDLPMVMGDRLHCMVLFATFTRVLGSSGLDTMTKTMEEKPMANPKKLYEPIVTT 1707
 Db 1668 lvmdlpmvseidrlhcmdilfaftarvlgsdgldsmkamemekfmeanplkklyepivtt 1727
 QY 1708 TKRKEEGGAIVIORAYKHEKVMKVLRLKDRSS-----SSHQVFCNGDLSLSDVAKVK 1761
 Db 1728 tkrkeergaailqkatrymmkvtkgdqgdqndlenghpsqltclngdlsfgevakg 1787
 QY 1762 VHND 1765
 Db 1788 vhd 1791
 RESULT 9
 AAW23994
 ID AAW23994 standard; Protein; 2016 AA.
 AC AAW23994;
 XX
 DT 06-JUL-1998 (first entry)
 XX Human hhl sodium channel protein.
 DE
 XX Ion channel; sodium channel; hhl; human; cardiac cell; heart;
 KW pacemaker; gene therapy.

XX Homo sapiens.
 OS WO9802040-A1.
 PN 22-JAN-1998.
 XX
 XX 04-APR-1997; 97WO-US05556.
 XX 17-JUL-1996; 96US-0682433.
 XX (MEDT) MEDTRONIC INC.
 XX Morissette J, Stokes KB;
 PI WPI; 1998-110247/10.
 XX N-PSDB; AAV09029.
 DR
 DR System for delivering genetic material to heart - comprises
 PT reservoir, catheter and optionally pacing electrode for delivering
 PT ion-channel protein, useful for, e.g. improving sensing by pacemaker
 XX
 PS Disclosure; Page 41-47; 73pp; English.
 XX
 CC This protein comprises the human hhl voltage-regulated sodium
 CC channel protein that can be used in a novel system for enhancing
 CC cardiac signal sensing by cardiac pacemakers through genetic
 CC treatment. A claimed system for delivering genetic material (GM)
 CC comprises a reservoir containing GM and a device for delivering it
 CC to myocardial cells (MC) at a specific location. The GM increases
 CC the amplitude of the cardiac signal, improving the signal-to-noise
 CC (S/N) ratio that is sensed by the electrode of a pacemaker. Also
 CC claimed are: (1) an implantable delivery system comprising a
 CC reservoir for GM which increases the expression of ion channels in
 CC MC and system for delivering this through a catheter, the tip of
 CC which engages MC at the chosen location, and (2) a system similar
 CC to (1) comprising a pacing electrode on an inner wall of the heart,
 CC close to the site where the GM is delivered. The system is used
 CC for delivery of an ion-channel GM which causes depolarisation of
 CC atrial and ventricular MC and improves the sensing of cardiac
 CC signals by the pacemaker and the S/N ratio of atrial P-waves. The
 CC preferred GM comprises DNA (see AAV09029) or RNA encoding hhl.
 XX Sequence 2016 AA;
 SQ

Query Match 51.4%; Score 4712.5; DB 19; Length 2016;
 Best Local Similarity 50.2%; Pred. No. 0;
 Matches 971; Conservative 281; Mismatches 434; Indels 247; Gaps 29;
 QY 15 NFRPFTSDSLAAIKKRIAOKER-----KSKDKAAAEPPRPQDLKASRLKPLVGD 69
 Db 12 srrftrfreslaalekrmaekqargsttlqesreglpeeeaprpqldlqaskklplygnp 71
 QY 70 PPELVTPLEDDLPYKDKHTFMVNLKRTTYRESAKRALFIILGFNPLRLSRILSRVHS 129
 Db 72 pqligepleddlpfstqktfvlhngktrfisaatnalyvlsfpfpvrraavkvlvhs 131
 QY 130 VFSMFIICTVIINCMFMANSMERSFDNDIP-----EYVFTGIYILBAVILKARGFIVD 183
 Db 132 lfmnlmctiltntcvfma-----qhdppptwkyveyftfaiytfeslvkilarafclh 184
 QY 184 EFSELRDPWNWLDIFVIGTAIATCFPGSQVNLSALRTFRVFRALKALISVLSGLAVIGAL 243
 Db 185 afflrpdpwnwldfsvlimayttfiv-dlgnvsalrtfrvrlalktisvlsigklvial 243
 QY 244 LRSVKLLVDVNVLTFLCLISIFALVGQOLFGLLNOKKILKHCNCPNA----- 290
 Db 244 lqsvkkladvmvltvfcslsvfaliqlfmgnlrhkvrnftalngtngsveadglvves 303
 QY 291 -----SNKDCFEEKSEDFIMCCTWLGSRPCPNNGSTCDKTTLPNDNNYTKDFNFGWSFL 345
 Db 304 ldlylsdpnyllkngtsvllcngssdagtcpegycclkagenpdbhgysfdfsawaf 363

Claim 31; Page - ; 76pp; English.

The present sequence is that of the claimed delF1617 mutant of the human SCN5A protein. The mutant is encoded by an SCN5A mutant gene carrying a deletion of the TTC codon for phe-1617. Mutations of the SCN5A gene are implicated in Romano-Ward syndrome, the autosomal dominant form of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene lead to the following amino acid alterations in the encoded protein: D1114N, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the mutations provides means for assessing a risk in a human subject for LQTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCN5A gene. Note: The present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence Listing (see AAB82220).

Query Match 51.4%; Score 4712; DB 22; Length 2015;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 972; Conservative 280; Mismatches 430; Indels 254; Gaps 30;

QY	15	NFRPFTSDSLAAIKKRIAIOKER-----KKSKDKAAAEPPQRPQDLKASRKLPKLYGDI	69
Db	12	sfrifreslaaelekmaeqarqsttlgesrigepeeearpqldlqaskllpdlgynp	71
QY	70	PPELVTKPLEDDPYKYDKHKTVMVLNKKRTIYRFSAKRALFILGPNFNLRLSLMRILVS	129
Db	72	pqeliegpleddlopystkftivlnkgkltlfrsatnalyfshpvrhaavkilvhs	131
QY	130	VFSNFIICITIIINCMFANSMERSFDNDIP-----EYVFIGIYILEAVIKILARGFIVD	183
Db	132	lfomllmctaltncvma-----ghdpppwtkyeyftaiytfesivkjarafelh	184
QY	184	EFSELRDPNNWLDIFYIGTAITATCFPGSQVUNLSALRTFRVFRALKRAISVIGCKVIVGAL	243
Db	185	aftlrdpwnldsfvilmayttetfv-dlgnvsalrtfrvlralktisvisglktivgal	243
QY	244	LRSVKVLVDVMVLTFLCSLFFALVGQOLPMGILNOKCIKHNGGNPA-----	290
Db	244	iqsvkkladvmvltvfcslvafaligqlfmgnlrhkcvrnfaltngtngsveadglvws	303
QY	291	-----SNKDCFEREKDSEDFIMCGTWLGRSPCNSTCDKTTINPDNNYTKFDNFCWSFL	345
Db	304	ldlylsdpenylikngtsdvlvcgnssdagtcpegycrlkagenpdhgytsfdfsawaf	363
QY	346	AMFRVMTQDSWERLYQOILRTSGIYVFVFVVYFVIGSFYLNLTAVVTMAYEBSQNRV	405
Db	364	alfrlatqdcwerlyqgtlrsagkiymifmivflgsfylnllavvmaeyesepqat	423
QY	406	AAETEAKEMFOBAQOALLBREKEALVAMGIDRSSLNSLOASFSF-----KRRKFFG	457
Db	424	iaeteekrfqeamelmkhealtlirgvdvtsrsslenslapvshertsrktrkms	483
QY	458	S-----KTRKS-----PFMRGSKTAQASA	476
Db	484	sgteecegdrlpkdsdeedpramhmlslrglrsrtsmkprsrsgsiffrldlsead	543
QY	477	SDSEDDASKN-----PQLEQTKRLSNLP-----	501
Db	544	addenstareshtsltlvpwplrrtsaqgqpsqptsapghalhgkknstvdvcngvysl	603
QY	502	-----VDLFDEHVDPLHRQ	515
Db	604	lgagdbeatspgshllrprvmlehpddtttpeepggpqlmtsqapcvdgdfee-----pgarq	660
QY	516	RAISAVSIILTITIOEKEFOECPFCGKNLASKYLVWDCSPOWLCTIKKVLRTIMTDPTE	575
Db	661	raisavsvltsaaleeleershkcpccwnrlagryliwecpcplwmslkggvgkivmmbptd	720
QY	576	LATIGCIINTVFLAVEHNNMDNLKTIILKIGNVFTGIFIAEMCLKIITALDPYHVRHG	635


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Db 1125 apgcgetpedssegstadmntaelleqipdlqgvkdbedcftegcvrrccpccavdt 1184
Qy 1014 KSPVVLWNNIRKTCYQVHKHSWPSFIIFVILLSSGALIFEDVNLPSRQVEKLLRCTDN 1073
Db 1185 qapgvwvrrlkrctyhivshswfctfiifmllssgalafediyleerktikvilevadk 1244
Qy 1074 IFTFILLEMLKVVAFGRFYFTSAMCWLDLIVVSVLSM-----NLPCLKSFRT 1126
Db 1245 mftyvfvlemlkvwavgyfkfncawcwlfdllyvslsvlantlfgaemgpikslrt 1304
Qy 1127 LRALRPLRALSOFGMKVYVVALISAIPAILNVLVLCILFWLFCILGNLFSKFGRCI 1186
Db 1305 lralrplralrsefegmrvvvalgaipsimvllvclfwlfsimgvnlfagkgrci 1364
Qy 1187 NGTDINMYLDFTEVPNRSOCNISNYS-----WKVQVNFNDVGNAYLALLQVATYKGLWEI 1242
Db 1365 nqtegdipnlytinnksqceslnltgelywtkvkvfnvfnvgagylallqvattfkvgvmdi 1424
Qy 1243 MNAADVDSREKDEOPDFEANYLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNOQOKKIGQD 1302
Db 1425 myaavdsrgyeedqpwynlymylyfviifiifgsfftlfnfigviidnfnqgkklg99qd 1484
Qy 1303 IFMTEEEKKYYNAMKLGTRKPKQPIPRPLNKCQAFVFDLVTQVDFVIIIGLILVNNII 1362
Db 1485 ifmteekkyynamkkgkpkqpiprlnkyqgfidvktqafvtimfliclmvt 1544
Qy 1363 MNAESAQPKDKVKTFDILNIAFVVIETIECLIKVFPALRQHYFTNGNLFPCVVVLSII 1422
Db 1545 mnvetddgsekinilaklnlifaiftgecivlaalrhyffenswnifvfvvilsiv 1604
Qy 1423 STLVSRLSDSDISPPPTLFRVRLRIGRILRLVRAARGIRTLFALMMSLPSLFNIGLL 1482
Db 1605 gtvisldiqk-yffsptlfrvirirgrilrigrakgrtlifaammslpalfn.9ll 1663
Qy 1483 LFLVMFYIYAFGMSWFSKVKKGSGIDDIFNFPETFTGSMCLCFQITTSAGWDTLNPMLE- 1541
Db 1664 lflvmfisyifgmanfaykvweagiddmfnftfansmclcfqittsagwdgllspilnt 1723
Qy 1542 AKEHC-----NSSQSDSQOQPIAVVYFVSYIIISLIVVNMVIAVILENFNTATSESE 1595
Db 1724 gpyyctplnpsngsrdcsdpavgilfftyiisflivnmvialilensfateest 1783
Qy 1596 DPLGEDDFEIFYEWEXFDPASOFIOVSALSDADALPEPLRVAKNKFQFLVMDLPMV 1655
Db 1784 eplsedfdmfeiwefidpeatfiesvlsdfadalseplrlakpnqislinmdlpmv 1843
Qy 1656 MGDRLHCDVLFATFTRVLGDSGLDTMTKMTMEKFMFANPKKLYEPVITVTKRKEEQ 1715
Db 1844 sgdrhcmldilfatkrvlgsgemdalikqmeekfmaanspkisyepitttlrrkheev 1903
Qy 1716 GAAVIOARXKHM 1728
Db 1904 samviqrafrthl 1916

```

RESULT 12

AAB82240
ID AAB82240 standard; Protein; 2016 AA.

AC AAB82240;

XX 21-JUN-2001 (first entry)

XX Human SCN5A mutant D1114N.

DE SCN5A; Long QT syndrome; LQTS; cardiovascular disease;

KW Romano-Ward syndrome; diagnosis; prognosis; therapy;

KW drug screening; mutant; muten.

OS Homo sapiens.

XX W0200124681-A2.

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XX 12-APR-2001.
PD 09-AUG-2000; 2000WO-US21660.
XX 09-AUG-1999; 99US-0147488.
PR 17-MAR-2000; 2000US-0190057.
XX (UTAH ) UNIV UTAH RES FOUND.
PA Keating MT, Splawski I;
XX WPI; 2001-290564/30.
XX New KVLQT1 and SCN5A genes, which contains alterations or mutations,
XX useful in diagnostic/prognostic or drug screening methods, particularly
XX in mutational analyses for screening individuals with or at risk for
XX long QT syndrome
XX Claim 31; Page -; 76pp; English.
XX The present sequence is that of the claimed D1114N mutant of the
XX human SCN5A protein. The mutant is encoded by an SCN5A mutant
XX gene in which a G/A mutation alters codon 1114 from GAC to AAC.
XX Mutations of the SCN5A gene are implicated in Romano-Ward syndrome,
XX the autosomal dominant form of Long QT syndrome (LQTS). Mutations
XX newly discovered in the SCN5A gene lead to the following amino acid
XX alterations in the encoded protein: D1114N, L1501V, delF1617,
XX R1623I, E1784K and S1787N. Knowledge of the mutations provides
XX means for assessing a risk in a human subject for LQTS, for
XX diagnosing a mutation which causes LQTS, and for screening for drugs
XX useful in treating a human having a mutation in the SCN5A gene.
XX Note: The present sequence is not shown in the specification but is
XX derived from the KVLQT-1 sequence given in the Sequence Listing
XX (see AAB82220).
SQ Sequence 2016 AA;

```

Query Match 51.4%; Score 4711.5; DB 22; Length 2016;
Best Local Similarity 50.1%; Pred. No. 0;
Matches 970; Conservative 279; Mismatches 433; Indels 255; Gaps 28;

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Qy 15 NFRPETSLSLAAIKKRTAIOKER-----KSKDKAAAEPPQRPOLDLKASRLKPLKYGDI 69
Db 12 sfrffreslaalekrmaekqargsttlqesreglbeeeaprpqldiqaskklpolygnp 71
Qy 70 PPELVTKPLEDLPYYKDKHTFMVLNKKRTIYRFSAKRALFILGFPNPLRLSMIRISVHS 129
Db 72 pqeligepleddpfystqktfivlnkgktifrsatnalyvlsfpfpvrraavkllvhs 131
Qy 130 VFSMFICTVTIINCMFANSMERSFDNDIP-----EYVFTGIYILRAVILARGFTVD 183
Db 132 lfnmlimctiltncvfma-----qhdppptkyveyfttaiyfeslvkilarafclh 184
Qy 184 EFSELRDPWNWLDLFIIVIGTAITATCFPGSQVNLSALRFRFRERALKASIVISGLKAVIGAL 243
Db 185 aftflrdpwnwldfsvlmiayttefv-dlgnvsalrtfrvrlralktisvsglktivgal 243
Qy 244 LRSVKKLVDVMVLTFLCLISIFALVGQQLFMGLNOKCIKHNKGNPNA----- 290
Db 244 lqsvkkladvnmvltvclsvfallglqlfmglnlrhkevrnftalngtngsveadglvwes 303
Qy 291 -----SNKDCFEKEKDESDIFMCGTWLGSRPCNGSTCDKTTTLNPDNNYTKFDNFGWSFL 345
Db 304 ldllylsdpenyllkngtsdvllcgnssdagtcpegycclkgapendgtytsdfsawaf 363
Qy 346 AMFRVMTQDSWERLYRQLIRTSGLIYFVFFVFWVFLGSFYLLNLTFLAVTWMAYEQNRNV 405
Db 364 alfrimtgdcwerlyyqgtlrsagkiymflmvlifslgfyvlnlilavvamayecqngat 423
Qy 406 AAETEAKEMKFOEAQQLLRKEKEALVAMGIDRSSLSNLQASSFSF-----KKRKFFG 457

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Db 424 iaeteekrfqeamemlkhealtirgvdtsrslslemplavpnsherrkrkms 483
Qy 458 S-----KTRKS-----PFMRGSKTAQASA 476
Db 484 sgteecgedrlpkdsedgpramhhlsltrgtsrsmkprsrsgsiffrirdlgseadf 543
Qy 477 SDESDASKN-----POLLEOTKRLSONLP----- 501
Db 544 addenstareshhtslvwprrtsaqgpgstsapghalhgnknstvdngvvs1 603
Qy 502 -----VDLFEHVDPLHRQ 515
Db 604 lgsdpeatspgshllrpvmlehpdpdtttseepgpgmltsqapcvdfee---pgar 660
Qy 516 RALSAVSILTTIOEQRFQPCPCGKNLASKYLWDCSPQWLCIKVLRTIMTDPRTE 575
Db 661 raleavsvltsaaleesrhkpcpwnrlagryliwecplwmsikgvgklvmdpftd 720
Qy 576 LAYTICIINTVLAVERHHNDDNLKTLTKIGNWVFTGIFTAECLKIIALDPVHYFRHG 635
Db 721 ltlmcivlntlfmalehymntsefeemlvgnlvftgftaentfklialdpvyfqq 780
Qy 636 WNVDSIVALLSLADVLNTLSDNRSFLASLRLVFEKLAKSWPTLTLKIIGHSGVA 695
Db 781 wniifdsiivlsmeigfmsrns--nlsvlrfrlrvfklakswptlntliikignsvga 838
Qy 696 LGNLTVLTIVVFISFVVMRLFGTKFNKTATAYATQERPRRRWHMDFVHSLVVFRLCG 755
Db 839 lgnltvlaliivfavgmgldfknyselr-dsdgllprwhmdffhafiifrlcg 897
Qy 756 EWENMGCMODGSPICIIIFVLIIMVIGKVLNLFIALLLNSFSNEEKDGLSEETR 815
Db 898 ewietmwdcm-evsgqslcllflvmvignlvlnflallssfaadnltapde-dre 955
Qy 816 KTKVQLADRRFRFAESFMLHALQSFCCCKCRK-----NSPKRKE 855
Db 956 mnnlqlalarlgrlgrkrttdfcgllhrpqkaalaaqgqlpsclatpysppppe 1015
Qy 856 TTESFAGENKDSILPDARPKREYDMDALYTGQAGAP---LAPLAEVEDDY--EYCGGG 910
Db 1016 tek-----vpptrketqfeegqpggtgdpvcpvpiavaesdddeeden 1065
Qy 911 ALPTSQHSAGVQAGDL-----PPTKQLTSDDQGVEMEVFESEDLHLS----- 954
Db 1066 slgteesskqdesqpsvgwprgppdstswq-----vsatasaeasasqanwrgqwk 1120
Qy 955 --IOSPRKKSDAVMSLSCSTIDLN---DIFRNLOKTVSPKKQDPDRCPFKGLSCHFLCHK 1009
Db 1121 aepqagcgetpedscesgscadmtntaelleqldlgdkdpcedctegcvrrcpcca 1180
Qy 1010 TDKRSPWLVWNNIRKTCYQIVKHSWFESFIIFVILSSGALIFEDVNLSPRPOVEKLLR 1069
Db 1181 vdtqagpkvwwlrktcyhivshswfetfiifmllssgalafedyileerkttkivlle 1240
Qy 1070 CTDNIETFIFFLEMLKWAFFGRYFTSAWCMWDLFLIVVVSLSM-----NLPSLK 1122
Db 1241 yadkmftyvfvlemlkwwavgyfkfncawcldflivdvslvslvantlgfaempik 1300
Qy 1123 SFRTLRALRPLRALSOFGMKVWVYVALISAPAILNLVLLVCLIFWLFCILGVNLFSGKF 1182
Db 1301 slrtlrailralsrfegmrvvvvvalvgaipsmnlvclflwifslmgvlnfadkf 1360
Qy 1183 GRCLNGTDINMYLDFTVPRNSOCNINYS----WKVPQVNFNDVGNVAYLALLOVATYKG 1238
Db 1361 grclnqtgedlplnytlvnnksqcsnltgelywtkvkvnfdnvgaylallqvattkg 1420
Qy 1239 WLEIMNAVDSREKDEQDFEALNYAYLYFYVFIIFGFFTLNLFIVGIIIDNFNOQKKL 1298
Db 1421 wmdlmyaavdrgyeegqgweynlymylyfvfiifgsfftlfnlfigvldfnqgkkl 1480
Qy 1299 GGQDIFTEEQKKYNNAMKKLGTKPKQIPRPLNKCQAFVLDVTSQVDFVILGLLVL 1358
Db 1481 gggd1fnteegkkyannamk1gskkpkp1prpinkyggf1d1vtdkqadvtimf1cl 1540

Qy 1359 NMIIMAESADQPKDVKKTFDILNIAFYVFIETIECLIKVFALRQHYFTNGNLFDCVVVV 1418
Db 1541 nmvmvmetddqspeklnlaklnllfvaiftgecivklaalrhyyftcnswnifdvv1 1600
Qy 1419 LSIISTLVSRLESDISFPPTPLFRVVRRLARIGRLRLVRAARGIRTLFLPALMMSLPSLFN 1478
Db 1601 lsiivgtvlsdlqk-yffsptlfrvirirgrirgagkirtlilfalmmlpalfn 1659
Qy 1479 IGLLFLVMFIYALFGMSWFSKVGSGIDIDIFENFETFTGSMCLCFQITTSAGWDTLLNP 1538
Db 1660 iglllflvmfiyslfgmanfayvkweagiddmfnfqtfansmclcfqittsagwdgllsp 1719
Qy 1539 MLE-AKEH-----NSSSDSCSQOQIAVYVFSYIIISFLIVVMYIAVILENFNAT 1591
Db 1720 ilnngppycdplnpsngsrgdcgspavgllfftyiisflivvmyiaillenfsvat 1779
Qy 1592 EESDPLGEDFEIFYEWEKEDPEASOFIOYSALSDFADALPEPLRVAKPNKQFLVMD 1651
Db 1780 eestplsedfdmfyeiwekfdeatfleysvlsdfadalseplriakpnqslimnd 1839
Qy 1652 LPMYMGDRLHCMVDLFAFTTRVLGDSGLDTMKTMMEEKFMEANPFKLYEPITVTTKRK 1711
Db 1840 lpmvsgdrhcmldlfaftkrvlgesgemdalkiqmeekfmaanspskisyepitttlrkr 1899
Qy 1712 EEEGAAVIOYRAYRKHM 1728
Db 1900 heevsamvigrfrrhl 1916

RESULT 13

AAB82245

ID AAB82245 standard; Protein; 2016 AA.

XX AC AAB82245;

XX DT 21-JUN-2001 (first entry)

XX DE Human SCN5A mutant S1787N.

XX KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
XX KW Romano-Ward syndrome; diagnosis; prognosis; therapy;
XX KW drug screening; mutant; muten.
XX OS Homo sapiens.

XX FN WO200124681 A2.

XX FD 12-APR-2001.

XX PF 09-AUG-2000; 2000WO-US21660.

XX PR 09-AUG-1999; 99US-0147488.

XX PR 17-MAR-2000; 2000US-0190057.

XX EA (UTAH) UNIV UTAH RES FOUND.

XX FI Keating WT, Splawski I;

XX PS WPI; 2001-290564/30.

XX DR New KVLQTL and SCN5A genes, which contains alterations or mutations,

XX PT useful in diagnostic/prognostic or drug screening methods, particularly
XX IT in mutational analyses for screening individuals with or at risk for
XX FT long QT syndrome
XX PS Claim 31; Page -, 76pp; English.

XX CC The present sequence is that of the claimed S1787N mutant of the
XX CC human SCN5A protein. The mutant is encoded by an SCN5A mutant
XX CC gene in which a G/A mutation alters codon 1787 from AGT to AAT.
XX CC Mutations of the SCN5A gene are implicated in Romano-Ward syndrome,
XX CC the autosomal dominant form of Long QT syndrome (LQTS). Mutations

newly discovered in the SCN5A gene lead to the following amino acid alterations in the encoded protein. D1114N, L1501V, delP1617, R1623L, E1784K and S1787N. Knowledge of the mutations provides means for assessing a risk in a human subject for LQTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCN5A gene. Note: The present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence listing (see AAB82220).

Sequence	2016 AA;
SQ	

Query Match	51.48;	Score	4711.5;	DB	22;	Length	2016;
Best Local Similarity	50.28;	Pred.	No. 0;				
Matches	970;	Conservative	281;	Mismatches	435;	Indels	247;
						Gaps	29;

QY	15	NFRPFTSDSLAAIKKRIAIOKER-----KKSKDKAAAEQPPRQQLDKASRKLPUKUYGDI	69
Db	12	sfrfrtslaaiekmaekqargsttlqesreglbeeeaprpqldlqaskllpdygnp	71
QY	70	PPELVTPLEDDLPYKDKHTEVMVLANKKRTIYRFESAKRALFILGPNPRLSRLMIRISVHS	129
Db	72	pqeligepledlpdyfstqtkfivlnkgkfciffsacnaalyispfhpvrreaavkllivs	131
QY	130	VFSFIITCIITINCMFANSWERSFONDIP-----EYFIGIYILEAVIKILARGFIYD	183
Db	132	lfmalmctiltncvfma-----qhdpppwtkyveytftalytfesivkilarafclh	184
QY	184	EFSLRPDWNWLDIVIGTIAITATCFPGSQVNLSALRTFRVFRALKAISVISGLKUVIGAL	243
Db	185	aftrfdpwnldfsvliamayttefv-dlgnvsalrtfrvtralktisvisgltktivl	243
QY	244	LRSVKKLVDMVWLTFLCLSIFALVGQOLFNGILNQKCIKHNCGNPA-----	290
Db	244	iqsvkkladmvtvltvclsvaligilqfmgnlrhkcvrnfaltngtngsveadglvwes	303
QY	291	-----SNKDFEKEKJSEDIFMCGTWLGSRPCNGSTCDKTTLPPDNNTYTKFDNFQWSFL	345
Db	304	ldylsdpnyllkngtstdvllcgnssdagtcpegycikagpenphgtytsfdsfawaf	363
QY	346	AMPRVMTQDSWERLYROILKTSIGYFVFPEVVVIFLGSFVLLNLTAVTMAYEQRNVV	405
Db	364	alfrimqcdwerlyqgtlrsagikymifmlviflgsyfvnlilavmayeeqngat	423
QY	406	AAETEAKEMFOEAQOQLLREEKALYAMGIDRSLSLQAASSPSP-----KKRKPFQ	457
Db	424	iaeteekefrgeamemlkehealtirgvdvtvsrslsmlsplayvnsherrskrrkms	483
QY	458	S-----KTRKS-----FPMRSGSKTAQASA	476
Db	484	sgteecgedrpkdsdsedgpramnhisltrglrtsmkprsrsgsiftfrirdlgsead	543
QY	477	SDSEDDASKN-----PQLEOTKRLSONLP-----	501
Db	544	addenstareshtslvvpwplrtrtsagqpsptsagphalhghkknstvdncgvvs	603
QY	502	-----VDLFDEHVDPLHRQ	515
Db	604	lgagdpeatpgshllrpvmlehpdtltptseepgpgqmltsaqpcvdgfee--pgarq	660
QY	516	RALSAYSILITITQOEKFOEPCFGCKNLASKYLVWDCSPQWLCKTKVLRTIMDPDFFE	575
Db	661	raisavsvltsaleejeesrhkcpccwnrlaqryllweccplwmsikggvklvmdpftd	720
QY	576	LAITICIIINTVFLAVEHHNMNDNLTKILIGNWFTGTFIAEMCKLIILADOPYHYFRHG	635
Db	721	ltitmcivlntlmalnyhmtsefeemlqvgnlvftgftaemtfkilalopyyfqg	780
QY	636	WNVPDSTVALLSADVLYNTLSNNNSRFTLASLRVLRFVKLAKSWPTLNTLIKIHSVGA	695
Db	781	wnfdsvlslvimejlglsrms--nlsvlrfsfllrvfkvlakswwptlntklignsva	838


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Db 1185 gapkvwwrlrktcyhivhswfetfiifmillssgalafediyleerktikvileayadk 1244
Qy 1074 IFTFTLEMLIKVAFGRFYFSAMCWLDFLIIVVSVLSIM-----NLPSLKSPRT 1126
Db 1245 mftyvfvlemllkwvaygfkfynawcwlflivdsvlsivtantlgfaemgpikslrt 1304
Qy 1127 LRALRPLRALSQFGMKVYVYALISAPAILNVLVLLVCLIFWLVFCILGNLFSGKFGRCI 1186
Db 1305 LRALRPLRALSRFEGMRVNVNALGALPSIMNVLLVCLIFWLVFCILGNLFSGKFGRCI 1364
Qy 1187 NGTDINMYLDTFVNPNSQCNISNYS-----WKVPOVNFNDVNGVAYLALLOVATYKGMLEI 1242
Db 1365 nqtegdplnytiavnksqcslnltgelywtkvkvnfdnvgagyallavvatfkgwmdi 1424
Qy 1243 MNAADVSRKDEQDPDFEALNAYLYFVVFIFGFSFFTLNLFIGYIIDNFNOQKKLGQD 1302
Db 1425 myaavdsrgyeegpqweynlymyfyvfiifgfsfftnlfigvldnfnqdkkklgqgd 1484
Qy 1303 IFMTEEQKYYNAMKKGTKRQKPIPRPLNKCQAFVFDLVTQVDFVILGLVLNMI 1362
Db 1485 ifmteeqkyyNAMKKGSKPKPIPRPLNKGQGFIDIVTKAFAVIMFLICLMVT 1544
Qy 1363 MNAASQPKDKVKTFTDILNFAVFIETIECLIKVFAIROHYFTNGWNLFCVQVVVLSII 1422
Db 1545 mmvetddgspekinilaklnilfvaiftgecivklaalrhyftnwnifdvfvvilsiv 1604
Qy 1423 STLVSRLSDSDISPPPTLFRVRLARIGRLRLVRAARGITLIFALMMSLPSLFNIGLL 1482
Db 1605 gtvlsldliq-yfssptlfrviriarigrilrlirgagirtlifaalmsipalnfagll 1663
Qy 1483 LFLVMFIAYIFGMSWFSKVKSGSIDIFNPFTFTGMLCLFQITTSAGWDTLLNPMLE- 1541
Db 1664 lflvmfiysifgmanfaykveagiddmfnqtfansmclcfqittsagwdgllsprint 1723
Qy 1542 AKEHC-----NSSQSDSCQOQIAVYVFSYIIISFLVVNMVIAVILENFTATBESE 1595
Db 1724 gpycdptlpnsngsrgdgsapvgilfftyiisflivnmvyaailenfsfvateest 1783
Qy 1596 DPLGEDPEIFVEYWEKEDPEASOFIOYSALSDFADALPEPLRVAKNPKFOFLVNDLPMV 1655
Db 1784 episeddmdfyeiwekfdpeatgfiesvlsdfadalseplrlakpnqislinmdlpmv 1843
Qy 1656 MGDRLHCHMDVLFATFTRVLGDSGLDTMKTWMEKFWMEANPFKKLYEPIVTTTKRKEEQ 1715
Db 1844 sgdrhcmldilfatkrvlgesgemdalikigmeekfmaanspskisyepitttlrrkheev 1903
Qy 1716 GAAVQIRAYRKHM 1728
Db 1904 samvigrarrrhl 1916

RESULT 15
AAB82244
ID AAB82244 standard; Protein; 2016 AA.
AC
AC AAB82244;
XX
XX 21-JUN-2001 (first entry)
DT
XX Human SCN5A mutant E1784K.
XX
XX SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy;
KW drug screening; mutant; mutain.
XX
OS Homo sapiens.
XX
XX WO200124681-A2.
XX
XX 12-APR-2001.
XX
XX 09-AUG-2000; 2000WO-US21660.
XX
XX

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PR 09-AUG-1999; 99US-0147488.
PR 17-MAR-2000; 2000US-0190057.
XX
XX (UTAH ) UNIV UTAH RES FOUND.
PA
XX Keating MT, Splawski I;
PI WPI; 2001-290564/30.
XX
XX New KVLQ1 and SCN5A genes, which contains alterations or mutations,
XX useful in diagnostic/prognostic or drug screening methods, particularly
XX in mutational analyses for screening individuals with or at risk for
XX long QT syndrome
XX
PS Claim 31; Page -: 76pp; English.
XX
XX The present sequence is that of the claimed E1784K mutant of the
XX human SCN5A protein. The mutant is encoded by an SCN5A mutant
XX gene in which a G/A mutation alters codon 1784 from GAG to AAG.
XX Mutations of the SCN5A gene are implicated in Romano-Ward syndrome,
XX the autosomal dominant form of long QT syndrome (LQTS). Mutations
XX newly discovered in the SCN5A gene lead to the following amino acid
XX alterations in the encoded protein: D1114N, L1501V, delF1617,
XX R1623L, E1784K and S1787N. Knowledge of the mutations provides
XX means for assessing a risk in a human subject for LQTS, for
XX diagnosing a mutation which causes LQTS, and for screening for drugs
XX useful in treating a human having a mutation in the SCN5A gene.
XX Note: The present sequence is not shown in the specification but is
XX derived from the KVLQ1-1 sequence given in the Sequence Listing
XX (see AAB82220).
XX
SQ Sequence 2016 AA;

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Query Match 51.3%; Score 4708.5; DB 22; Length 2016;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 970; Conservative 280; Mismatches 436; Indels 247; Gaps 29;

Qy 15 NFRFTSDSLAAIKRTRAIQKER-----KSKDKAAAEPPQRPQDLKASRKLPLKYGDI 69
Db 12 sfrftreslaaiekrmaekdargsttlqesreglpeeeearpqldiqaskklpolygnp 71
Qy 70 PPELVTPKPLEDLPYVDKHTFMVLNKKRTIYRFSAKRALFILGFNPNLRLSLMTRISVHS 129
Db 72 pqeligepleddpfystqtkfvlngkgtlfrfsatnalyvlspfpvrraavkilvhs 131
Qy 130 VFSMFIITCTVIINCMFMANSMERSFNDIP-----EYVFIGIYLEAVIKILARGFTVD 183
Db 132 lfnmlmctiitncvfma-----ghdpppwtkyveyftaiytfeslvkilarafclh 184
Qy 184 EFSFLRDPWNWLDIFIVIGTATATCFPGSQVNLSALRFRFRFRALKATISVLSGLKIVIGAL 243
Db 185 aftfirdpwnwldfsvliamayttefv-dlgnvsalrfrvrlraiktisvlsigklvlgal 243
Qy 244 LRSVKKLVDVWMLTFLCLISIFALVQOQLFMGILNOKCKIKHNGPNPA----- 290
Db 244 lqsvkkkadvmvltvfcslsvfaliglqlfmgnlrhkvrnftalngtngsveadglvwes 303
Qy 291 -----SNKDCFEKEKDESDIFMCGTWLGSRPCNGSTCDKTTLPNDNNYTKDFNFGWSFL 345
Db 304 ldllylsdpenyilkngtsdvllcngssdagtcpegycclkgapndhgytfsdfawaf1 363
Qy 346 AMFRVMTQDSWERLYRQILRTSGIYFVFFVVFVFLGSFYLLNLTAVTWMAYEEQNRNV 405
Db 364 alfrimgdcwerlyqgtlrsagkiymifnlviflgsfylnlilavvamayeegndat 423
Qy 406 AAETEAKEMFOEAQQLLREEKEALVAMIDRSLSNLSQASSFSF-----KKRRPFG 457
Db 424 iaeteekkrfqeamemlkkhealtirgvdtsrslslemaplavpnsherrkrkrms 483
Qy 458 S-----KTRKS-----KTRKS-----FFMRGSKTAQASA 476
Db 484 sgteecgedrlpksdsedgpramnhlsitrgltsmtsmkprsrsgsiffrirdlgseadf 543

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Qy 477 SDSDDASKN-----PQLEQTKRLSQNLUP----- 501
Db 544 addenstareshtsallvwprrtsagqpspgtsapghalhgnkstvcngvvs1 603
Qy 502 -----VDLDEHVDPLHRQ 515
Db 604 lsgadpeatspgshllrpvmlehpddtttseeppgpmiltsqpcvcdgfee---pgar 660
Qy 516 RALSASILITITIOEQKFQPPCCGKNLASKYLVWDCSPQWLCKIKVLRITIMTDPTTE 575
Db 661 ralsavaltaleeleeshkpcpcwnrlaqryliwecplwmsikgkvkvmvdpftd 720
Qy 576 LATIICIIINTVFLAEBHHNDDNLKYLKIGNWVFTGIFTAEMCLKIIALDHPHYPRHG 635
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Qy 816 KTKVQALDRFRRAFSFMLHALQSFCCCKCRK-----NSRPKE 855
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Qy 957 SPRKSDAVSMLSCSTIDLN---DIFRNLOKTVSPKKQDRCPKGLSCHFLCHKWDKR 1013
Db 1125 apggetpedscesgstadmtntaellieqldlgdgdpedctegcvcrrpcocavdt 1184
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Db 1185 qapgvvwrkrktcyhivenswfcfflmlssgaiafediyleerktikvleyadk 1244
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Db 1245 mftyvfvlemlkwwaygfkfytnawcwidflivdsvlsvlantlgfaemgpikslrt 1304
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Db 1305 lralrplraisrfegmrvvvnalvgaipsimvnlvclifwlfsimgvnlfagkgfrci 1364
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Search completed: February 27, 2002, 01:27:43
Job time: 10093 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2002, 22:39:50 ; Search time 61.5 Seconds
(without alignments)
645.826 Million cell updates/sec

Title: US-09-646-224A-2

Perfect score: 9173

Sequence: 1 MEERYVPVIFPDERNRPFTVFCNGDLSSLDVAKVKVHND 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4669.5	50.9	1956	4	US-08-843-417-10
2	4562	49.7	1969	3	US-08-836-325-16
3	4541.5	49.5	1984	3	US-08-836-325-10
4	4508.5	49.1	1989	3	US-08-836-325-12
5	4506	49.1	1956	4	US-08-843-417-2
6	4479.5	48.8	2005	3	US-08-836-325-7
7	4394.5	47.9	1978	3	US-09-024-0208-3
8	4390.5	47.9	1988	3	US-09-024-0208-4
9	4388.5	47.8	1989	3	US-08-836-325-11
10	4316.5	47.1	1976	3	US-09-024-0208-9
11	4185	45.6	1835	3	US-08-836-325-15
12	3554.5	38.7	2105	2	US-08-808-793-3
13	3554.5	38.7	2105	3	US-08-772-512A-3
14	3550.5	38.7	2104	2	US-08-808-793-4
15	3550.5	38.7	2104	3	US-08-772-512A-4
16	3532	38.5	2100	2	US-08-808-793-23
17	3532	38.5	2100	3	US-08-772-512A-19
18	3242.5	35.3	1820	3	US-07-998-289B-8
19	2593	28.3	1011	3	US-08-836-325-2
20	2085.5	22.7	813	3	US-08-836-325-8
21	1505	16.4	1872	6	5386025-6
22	1497.5	16.3	1873	1	US-08-435-675B-4
23	1488	16.2	2161	1	US-08-455-543A-51
24	1488	16.2	2161	2	US-08-223-305C-48
25	1487.5	16.2	1873	1	US-08-336-257A-7
26	1480	16.1	2161	1	US-07-745-206A-2
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28	1480	16.1	2161	2	US-08-223-305C-49
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43	1404	15.3	2509	2	US-08-149-097D-35
44	1306	14.2	452	3	US-07-998-289B-6
45	1187	12.9	413	2	US-08-808-793-25

ALIGNMENTS

RESULT 1

US-08-843-417-10

Sequence 10, Application US/08843417

Patent No. 6184349

GENERAL INFORMATION:

APPLICANT: Herman, Ronald C

APPLICANT: Delgado, Stephen G

APPLICANT: Fish, Linda M

APPLICANT: Sangameswaran, Lakshmi

APPLICANT: Rabert, Douglas K

TITLE OF INVENTION: CLONED PERIPHERAL NERVE

TITLE OF INVENTION: TETRODOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe

STREET: 525 University Ave

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.A.

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/843,417

FILING DATE: April 15, 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796

REFERENCE/DOCKET NUMBER: 28340-P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)-324-7041

TELEFAX: (415)-324-0638

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1956 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-843-417-10

Query Match 50.9%; Score 4669.5; DB 4; Length 1956;
Best Local Similarity 51.1%; Pred. No. 0;

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-16

Query Match 49.78; Score 4562; DB 3; Length 1969;
Best Local Similarity 49.98; Pred. No. 0;
Matches 961; Conservative 281; Mismatches 454; Indels 230; Gaps 34;

Qy 11 PDENFRPFTSDSLAAIKRIAIOKERK-KSKDAAABPOPPOLDLKASRLPKLYGDI 69
Db 7 PGOSFVHTKQSLALTEORAEKSKPEKEKDDDEAPKPSDLEAGKQLFFIYDI 66

Qy 70 PPELVTKPLEDDPYKDKHTFMVNLKRTIYFSAKRALFILGPNPLSLMIRISVHS 129
Db 67 PPGMVSEPLEDDPYADKTFIVLNKGAIFRENAFALYMLSPFSLRISIKILVHS 126

Qy 130 VFSMFICTVILNCFMANSRERFDNDIPYVIGIYILAVIKILARGIVDEFSLR 189
Db 127 LFSLMILCTILNCFIMNPPDWTKNV-GYTFGTIYFESLVKILARGFCVGEFTLR 185

Qy 190 DPWNMLDFIVGTATATCFPGSQVNLASALRFRVFRALKATISVGLKIVIGALLRSVKK 249
Db 186 DPWNMLDFIVFAYLTFEV-NLGNVSALRFRVLRALKTISVPLGLTIYVGLIISQVKK 244

Qy 250 LVDVWVLTFLCSIFALVQOGLFMGLNKGKCIKHCNPNPA--SNKDCFEKEK----- 301
Db 245 LSDVMILTVCLSVFALIGLQFMGLNKGKCFRNLNENETLESIMNTLESEEDFRKYFY 304

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Db 305 YLEGSKDALLCGFTSDGQCPEGYTCVKIGRNPDPYGYTSDFTSWAFLALRLMTQDYWE 364

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Db 365 NLYOQTLRAAGKTYMIFVVFVIFLGSFYLLNLTAVVTMAYEEQNRNVAAATEAKEMFO 424

Cy 418 EAQQLLR--EEKEALVA-----MGIDRRSLNSLQASSFPKRRKFGSK-- 459
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Cy 460 -----TRKSFPM----- 466

Db 485 QKLLSGEEKGDAEKLKSKSESDSIRRSKSFHLGVGCHRAHEKRLSTPNQSPLSIGSLF 544

Cy 467 ---RGSKT-----AQASASDSE-----DDASKNPQL-----LEQ 492

Db 545 SARSSRTSLSFKGRGRDXGSETEFADDEHSIFGDNESRRGSLFVPHRPXERRSNISQ 604

Cy 493 TKRLSONLPVD-----LF 505

Db 605 ASRSPMLPVNGKMHSAVDCNGVSLVDGXSAALMNPGLPEGTNQIHKRRKSSYLL 664

Cy 506 DEHV--DPLHRORALSAYSILTIIOEQEKFOEPCFPCKKNLASKYLWDCSPQWLCKKK 563

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Cy 624 IALDPYHYFRHGNVDFDSIVALLSLADVLYNTLSD--NNRSFLASLURVLFKLSWPTL 682

Db 785 IAMDPEYFQVGNIFDSLIIVTSLVELF---LADVEGLSVLSRFLRLRVFKLSWPTL 841

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Cy 802 SNEEKDGSLEGETRKTQVQLADLDRFRRAFSPMLHALQSCCKKRRKNSPKPKETTESFA 861

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Db 1016 AE-----DNTKKENTISNMTLAEMSKG---HNFLKEKDKISGSGSXKHLMEDSDG 1065

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Db 1066 QSFTHNPSTVTVIAPGESLDMNEELSSDSD---SYSKNRSS-----SECTVDNP 1116

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QY 1738 DRSSSS 1743
Db 1890 VKNISS 1895

RESULT 3

US-08-836-325-10
; Sequence 10, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203.
REFERENCE/DOCKET NUMBER: 0917.02400002.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-10
Query Match 49.5%; Score 4541.5; DB 3; Length 1984;
Best Local Similarity 48.9%; Pred. No. 0;
Matches 954; Conservative 291; Mismatches 443; Indels 263; Gaps 35;
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Db 127 LFSMLIMCTILTNCFMILSNPPETKNV-EYTFGTIYTFESLIKILARGEVGVGFTFLR 185
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Db 245 LSDVMILTVCLSVFALIGLQLFMGNLKHKCFKELENETLESTMTAEEELKKYFY 304
QY 302 ----SEDFIMCGTWLGRPCNGSTCDKTTLPDNNYTKFDNFGWSFLAMFRVMTQDSWE 357
Db 305 YLESGKDALLCGFSQDQCEGYICVAGRNPDYGTSTFDTFSWAFALFRIMTQDYWE 364
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QY 418 EAQOLLR---BEKEALVA-----MGIDRSSLSLQASSFSFKKR-----453
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QY 454 -----453
Db 485 QKMSGEEKGDDEKLKSGSSESIKKSFHILGVEGHHTREKRLSTPNQSPLSIRKSLFS 544
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Db 545 ARRSRTSLFSFKGRDLGSETEFADDEHSIFGDNESRRGSLFVPHPRRRSSNLSQA 604
QY 475 SASD-----SEDDASKNPOLL 490
Db 605 SRSPVLPVNGKMHSAVDCNGVSLVDGPSALMLPNGQLPEVIIDKATSDSGTTNQ- 663
QY 491 EOTKRLSON--LPVDLDFEHVDPLHRQALSAVSLITITIOEQEFQPCPCGNLASK 548
Db 664 -RKRLSSSYFLSEDMLN---DPLHRQAMSRASILTNTVEELESROKCPWPWYRFHT 719
QY 549 YLVWDCSPQWLCIKKVLRTIMTDPTELAITICIIINVLAVEHNNDDNLKTLKICN 608
Db 720 FLINWCSYWLKFKKLIYFIVWDFVDLAITICIVNLTFMAHEHPTEFEKNVAVGN 779
QY 609 WFTGIFTAEMCLKIIALDPYHYFRHGNVFDISVALLSLADLYNTLSD--NNRSFLASL 667
Db 780 LIFTGIFAAEMVLKLIAMDPEYFQVGNIFDLSLITVLSLITFELF---LADVEGLSVLRSF 836

QY 130 VFSMFIICVTIINCMMFMANSMERSFDMNDIPEYVFIIGVILFAVILKILARGFIVDFEFLR 189
Db 127 LFSMLIMCILTILNCIEFTLSNPPETKNV-CYTFGTIYTESLIKILARGCEVGFELR 185
QY 190 DPNWNLDFIVIGTAIATCFCGSGQVNLGALTRFRVFRALKALISVTSGLKIVIGALLRSVKK 249
Db 186 DPNWNLDFIVIVFAYLAEFV-NLGNVSALRTRFRVLKALTSIVPGLKTIIVGALIQSVKK 244
QY 250 LVDVWMLTFLCLSFALVGQOLFMGILNOKCIKHNCGNPNA--SNKDCFKEKD----- 301
Db 245 LSDVMILTVFCLSVFALIGLQFMGNLKHCKFRKELENETLESIMNTAEEBELKYFY 304
QY 302 ----SEDFIMCGTWLGRPCNGSTCDKTLNPDNNYTKFDFNCFWFLAMPRVMTQDSWE 357
Db 305 YLESGKALLCGFTDSQCEGIVCVKAGRPDYGTISPTFSWALFALRMTQDIWE 364
QY 358 RLYQOILRTSIYVFFVFFVIFGFSYLLNLTLAVVTMAYEQNRNVAATEAKERMFO 417
Db 365 NLYOOTLRAAGTYMIFVFFVIFLGSFYLLNLILAVVAMAYEQNANIEAKOLEFEQ 424
QY 418 EAQOLLR---EKEALVA-----MGIDRSLNSLOASSPSPKKR----- 453
Db 425 QMLDLRAKEQEAIAAAAAAEFTSIRRSIRMGUSESSSETSRUSSAKERRNRKKK 484
QY 454 ----- 453
Db 485 QKXSSGEEKGDEKLSKSGSEESIRKSPHGLVGEHRTREKRLSTPNOSPLIRGSLF 544
QY 454 -----KFGSKT-----RKSPFM-----RGSRTAQ 473
Db 545 SARSSRTSLFSFKGRGRDLGSETAFADDEHSIFGDNESRRGSLFVPHRRPRRSSNISQ 604
QY 474 ASASD-----SEDDASKNPOL 489
Db 605 ASRSPVLPVNGKMHSAVDCVGVVSLVDGFSALMLPNGQLLPEVIIDKATSDSDGTTNOM 664
QY 490 LEOTKRLSON--LPVOLDDEHVDLPHRQRLASVSLITITIQEQKQEPFCPOCKNLAS 547
Db 665 --RKRLSSSYFLSEDMLN--DPLRQRAMSRASILTNTVEELESQRKCHQLLYRFAX 719
QY 548 KYLVWDCSPQWLCKKVLRTIMTDPFTELATITCIITVFLAVEHNMNDNLTKILIG 607
Db 720 TFLWNCSPWIKFKLITVIMDPFVDLAIITCIVLNTLFMAHEHPMTPEEFKNVLAVG 779
QY 608 NWVTFGIFAEMLCKIILADPYHYFRHCWNVDSIVALLSLADLYNTLSD--NRRSFLAS 666
Db 780 NLIFTGIFAEMLKILAMPDYEFGWNIFFSLIWLTSIELF---LADVEGLSVRS 836
QY 667 LRVLRFKLSKSWPTNLTKIIGHSVGALGNLTVLTIVVIFSVGMRLFGTKFNK-T 725
Db 837 FRLLRFKLSKSWPTNLTKIIGSVGALGNLTVLAIIIVFPAVVGMLFGKSYKECV 896
QY 726 AYATOERPRRWMDNEHYHSLVFLVFRILCGEWIENMGCMQMDGSPLCIIVFLIIVIG 785
Db 897 CKINVDCKLPRWMDNEHYHSLVFLVFRILCGEWIETMWDGM-EGVQTMCLITVMMVWIG 955
QY 786 KLVVNLFIALLNSFNEKDGSLGEGTRKTKVOLALDRFRFAFSFMLHALQSFCKKC 845
Db 956 NLVNLFIALLNSFSSDNLTAIEEDTDANNQIAVARIKRGINVKOTLREFILKSF 1014
QY 846 RRKNSPKPKETTESFAGEN--KDSILDPARPKWEYDTDMALYTOGAGAPLAPAEVEDDY 903
Db 1015 SKK--PKGSKDKTRTADPNKKNYISN-----RTLAEMSKDH 1050
QY 904 EY-----CGEGALPTSQHSAGVQAGDLPPETKQLTSPPDQG-VMEVEFSEEDLHLSI 955
Db 1051 NFLKEKDRIGSGSLDKSPMDENDYOSFTHNPSTVTVPIAPGESLEIMNTLEELSSDS 1110
QY 956 QSP--RKKSADVAMLSSECTID--LNDIFRNLQKTVSPKQPDRCFPKGLSCHFLCHTKD 1012
Db 1111 DSDYSKEKRNRSSSECTVDNPLPGEXEAEAEFPVNADEACFTDGCVRFPCCQVNV 1170
QY 1013 RKSPWLVWNIIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPOVEKLLRCTD 1072

Db 1171 DSGKGVWMTIRKTCYRIVBHSWESFIVLMILLSSGALAFEDIVIEKKTKIILEVAD 1230
QY 1073 NIFTFIFLEMLKWAFFPRRYFTSACWCLDFLIVVSVLSLM-----NLPSLKSPR 1125
Db 1231 KIFTYIFILEMLLKWAYGYKTYFTNACWCLDFLIVDVSLVTLANTLGYSDLGPISLR 1290
QY 1126 TLRALRPLRALSQFEGKVVVYALISAPAILNVLVLCLEFVLFCILGVNLFSGKFGRC 1185
Db 1291 TLRALRPLRALSREGEKVVVYALISAPAILNVLVLCLEFVLFCILGVNLFSGKFGRC 1350
QY 1186 INGTDINMYLDFTEVPRNSQC-----NIS-NYSWKVPQVNFNNGVNAVYLLALQVARYKWL 1240
Db 1351 VNTDGSRF-PTSQVANSRECEFCALMNVSGVNRKLNKVNFDVNGVLGYSLLQVATFKGM 1409
QY 1241 EIMNAVDSREKDEQDFEANYLAYLVFVFIIFGSFETLNLFIIGVIIDNFNOQKKLGG 1300
Db 1410 DIMYAAVDSVNVNEQPKYEYSLYMYIVFVFIIFGSFETLNLFIIGVIIDNFNOQKKLGG 1469
QY 1301 QDIFMTBEOKKYNNAMKLGTKPKQPIPRPLNKQAFVFDLVTQVDFVILGLIVLNM 1360
Db 1470 QDIFMTBEOKKYNNAMKLGSKPKQPIPRPGNKFPQGCIFDLVTNQAFDITIMVLICUNM 1529
QY 1361 IIMMAESADQPKVKKTFDILNIAFVWIFTIECLIKVFPALRQHYFTNGWNLFDQVWVLS 1420
Db 1530 VTMVKEGOTEYMDYVYLHWINMVFIILFTGECVLKLSLRHYFTVGVWNLIFYVWVLS 1589
QY 1421 IIST-LVSRBDSISPPPTLFRVVRVLRARIGRILRVRARIGRITLLFALMMSLPSLNI 1479
Db 1590 IVGMFLAEMIEKYFVS--PTLFRVIRLARIGRILRVRARIGRITLLFALMMSLPSLNI 1647
QY 1480 GLLLFLVWFIYAIFGMSWFSKVKKSGIDDLNFETFTGSMCLCFQITTSAGWDTLLNPM 1539
Db 1648 GLLLFLVWFIYAIFGMSNFAYVKEAGINDMNFETFGNSMCLCFQITTSAGWDTLLNPM 1707
QY 1540 LEA-----KEHCNSSQSCQPOQAVVYFVSYIISLIVVNMVIAVILENFAT 1591
Db 1708 LNSAPPDCPKKHPGSSVEGDCGNPSVGIFYFVSYIISLIVVNMVIAVILENFAT 1767
QY 1592 BESEDPGEDDFEIFYEWKEKFDPEASOFIOYALSDFADALPEPLRVAKPNKQFLVMD 1651
Db 1768 BESEDPGEDDFEIFYEWKEKFDPEASOFIOYALSDFADALPEPLRVAKPNKQFLVMD 1827
QY 1652 LPMVGRDLRCHMDVLAFTVRLVGLDSSGLDQTMKMEKFMENPFKLYPIVTTTKRK 1711
Db 1828 LPMVGRDLRCHMDVLAFTVRLVGLDSSGLDQTMKMEKFMENPFKLYPIVTTTKRK 1887
QY 1712 EEOGAAVIOYARKK-----HMEKMKVLRKL 1738
Db 1888 QEEVSATIIQYRRYRLRQHVKNKNISSYIKD 1919

RESULT 5

us-08-843-417-2
Sequence 2, Application us/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Deigado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
STREET: Heller Ehrman White & McAuliffe
ADDRESS: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843.417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: dorsal root ganglia
CELL TYPE: peripheral nerve
US-08-843-417-2

Query Match 49.1%; Score 4506; DB 4; Length 1956;
Best Local Similarity 50.7%; Pred. No. 0;
Matches 962; Conservative 269; Mismatches 443; Indels 222; Gaps 38;

Qy 15 NFRFTSDSLAAKRIAIQERKSKDAAAEE----PQRPQLDLKASRLPKLYGDP 70
Db 12 NFRFTPSLAEIEKQIAAARAAKARTKRGQEDKGKPRQLDLKACNOLPKFYGLP 71
Qy 71 PELVTKPLEDDPYKDKHTFWLNKRTIVRFSAKRALFLILGPNLRLSIRSVHSV 130
Db 72 AELVGEPLDDPYSTHRTFWLNKRTISRSATWALWLFSPNLRLTAIKSVHSV 131
Qy 131 FSMFICITVINCMPMANSERSFNDIP---EYVFIGIYILEAVIKILARGFVDFERSF 187
Db 132 FSIPTITILVNCMTRT-----DLPEKVEYVFTVITFEALIKILARGFCLNEFTY 184
Qy 188 LRDPMNLDFIVIGTAITCPGSOVNL---SALRTFRVFRALKAISVISGLKVIIVGALL 244
Db 185 LRDPMNLDFSVITLA-----YVGAIDLRGISGLRFRVLRALKTVSVIPGLKVIIVGALI 240
Qy 245 RSVKRLVDVMTLFLCLSFALVGQOLPMGLNOKIKHNGCPNPASNKDCFEK----- 299
Db 241 HSVKRLADVTILTVFCLSVFALVGLQLFKGNLKNKICIRNGTDPHKADNLSEMAEYIFIK 300
Qy 300 KDSDFIMCGTWLGRPCNGSTCDKTLNPDNNYTKEDNFCWSFLAMFRVMTQDSWRL 359
Db 301 PGTTDPLLCGNSDAGHCPGGVCLKTPDNPDFNTSETSDSAWFLSLFRLMTQDSWRL 360
Qy 360 YRQILRTSGITVFVFFVVFVIFLGSFYLNILAVVVMAYEQBNRVAETAERKMFQEA 419
Db 361 YQOTLRASGKMVMVFVIFLGSFYLNILAVVVMAYEQSOATAEIEAKEKFFQEA 420
Qy 420 QOLLREEKALVAMGIDRSSLSNLSQASSFSP-----KKRKFSG----- 458
Db 421 LEVQKEQEVJAAUGIDITLSQSHSGSLASKNANRRPRKRSVSEGSTDDNRSPPQSDP 480
Qy 459 ---KTRKSPFMRSKTAQAS-----ASDSED----- 481
Db 481 YNORMSFLGLSGRRRASHGVFHRAPSQDISPPDGTDDGVPHGDOESPRGSIILGR 540
Qy 482 -----DASKNP-----OLLEQTKRLSNLNP-----VDLDFEHV----- 509
Db 541 GAGOTGPLRSPPLQSPNPGRRHGEGLGVPTGELTAGAPEGPALDTTGOKSFLSAGYL 600

510 -DPLHRQALSAVSILITITIQEQRFBQPCPCGKNLASKYLWDCSPQWLCIKKVLRTI 568
Db 601 NEPPRAQRAMSVSVTMSVIELEBSKLPCLISFAQKYLWECCKPKWRKFMALFEL 660
Qy 569 MTDPTELAIYICIIINTVFLAVEHHNMDNLKTTILKIGNVVTGIFTAEMCLKIIADP 628
Db 661 VTDPEALTITLCIVVNTVFMAHYPMTDAFADLQAGNIYVTFVTMEAFKIIAEDP 720
Qy 629 YHPRHGNVFDSDIVALLSLADVLNLTSDNNRSFASLRLVRVFKLAKSWPTLNTLKI 688
Db 721 YYYFOKKWNIIFDCVITVTSLEL--SASKGSLSVLRTFLRLVRFKLAKSWPTLNTLKI 778
Qy 689 IGHSVGA LGNLTWLTIVVIFSVVMRLFGTKE--NKTAYATQPRRRRRHMDNFYHSF 746
Db 779 IGNSVGA LGNLTFILAIIVFIFALVGKQLLSESDYCRKDGVSVMNGEKLWMCDFHSHF 838
Qy 747 LVVFRILGWIENWMCQMDGSPICITIVFLVLTWIKLVVNLFTALLNSFSNE-- 804
Db 839 LVVFRILGWIENWMCQMDGSPICITIVFLVLTWIKLVVNLFTALLNSFSADNL 897
Qy 805 ---EKDGSLEGETRKTQVQLALDRFRRAFSFMLHALQFCCCKKRRKNSPKKETE--- 858
Db 898 TAPEDDGEV-----NNLQALARIQVIGHRASRAIASYISSHCRFR---WPKVETQLGM 948
Qy 859 ---SPAGENKDSILPDA-----RP-----WKBYDTDMALYTGQACAPLA--- 894
Db 949 KPPLTSSEAKNHIATDAVSAAGVNLTKPALSFPKENGHGDFTIDPNVW---VSVPTAEGES 1005
Qy 895 PLAEVEDDVEYC-----GEGALPTSQHSAGVOAGDLPPETKOLTSPDQGVBM 943
Db 1006 DLDELEDEMEQASQSSWOEDPKGOEQLPQVKCKENHQAARSP---ASMSEDILAPYLG 1063
Qy 944 EVFSEDLHLSTQSPRKSDAVSMLESGTIDLND---IFRNLQKTVSPKKOPDCRCPKG 1000
Db 1064 ESWKRKD---SPQVPAEGVDDTSS--SEGSTVDCPOPEELRKIPELADLDEPDCFTG 1119
Qy 1001 LSCHFLCHKTDRKSPVLMWNIRKTCYQIVKHSFESFIFVILLSSGALIFEDVNLPS 1060
Db 1120 CTRRCPCCNVNTSKSPWATGQVKTCTYIVHSFESFIFVILLSSGALAFEDNYLEE 1179
Qy 1061 RPQEKLLRCTDNITFFILLEMILKLVAFGRPRYFTSAWCWLDLFIIVVSVLSLM--- 1116
Db 1180 KPRKSVLEYTRDVTFTFVFEMLLKLVAYGFKYFTNAWCWLDLFIIVNISLTIK 1239
Qy 1117 ---NLPSLKSFTLRALRALSQFEGMKVVVYALISAIPAILNVLVLCFLFVLCIL 1173
Db 1240 EYSDVASIKALTRLRALRALSREFGRVVRVVDLVAIPAISIMNVLVLCFLFVLSIM 1299
Qy 1174 GYNLFSGRFGRCINGTDINMY--LDFTVPPNRSCNIN---YSWKVPOVNFNDVGNAY 1227
Db 1300 GYNLFAKFSKVD--TRNPPFSNVNTWVNNKSECHNQNSTGHFFWVNVKN-----Y 1351
Qy 1228 LALLQVATYKGLWEIMNAAVDSREKDEQDFPEANLYAYLYFY-----VFIFGSFETL 1280
Db 1352 LALLQVATFKGMDIWAADVDSGEINSQPNWNNLYMYLYFVFDVNVAMGVFIIFGFPFL 1411
Qy 1281 NLFVGIIDNFNOQKGLGGQDIFMTEBQKYKNAMKLGTKKPKOKPPIPRPNLKNQCAFV 1340
Db 1412 NLFVGIIDNFNOQKGLGGQDIFMTEBQKYKNAMKLGTKKPKOKPPIPRPNLKNQCAFV 1471
Qy 1341 DLVTSQVDFVILGLIIVLNMIIMAESADQPKDVKTDFILNIAFVIFTIECLIKVPAL 1400
Db 1472 DLVTSQVDFVILGLIIVLNMIIMAESADQPKDVKTDFILNIAFVIFTIECLIKVPAL 1531
Qy 1401 ROHYETNGNLDVGVVVLSTIISLVSIR--LEDSDISFPPFLFRVRLARIGRLIRLRAA 1459
Db 1532 ROHYETNGNLDVGVVVLSTIISLVSIR--LEDSDISFPPFLFRVRLARIGRLIRLRAA 1591
Qy 1460 ROIRPILLFALMMSLSPLNIGLILLFLVMPFIYAFQMSWFSKYGSGIDDIENFETFGS 1519
Db 1592 KGIRTLFALMMSLSPLNIGLILLFLVMPFIYAFQMSWFSKYGSGIDDIENFETFGS 1651

Qy 1520 MCLCFQITTSAGWDTLLNPMLE-AKEHC-----NSSQDSQOQIAVAVVFSVVIISF 1572
Db 1652 MCLCFQITTSAGWGLSPILNPPYCDPLNPNNSGRGCGSPAVGIIFFTHYIISF 1711
Qy 1573 LIVNMYIAVILENFNTATESEDDPLGDDFEIFYEWEKEDPEASQIOYSALSDFADA 1632
Db 1712 LIVNMYIAVILENFNTATESEDDPLGDDFEIFYEWEKEDPEATQIAFSALSDFADT 1771
Qy 1633 LPEPLRVAKPNKQFLVMDLPMVAGDRLHCDVLFAPFTTRVLGSSGLDTHKTMEEKFM 1692
Db 1772 LSGPLRPKPNQNTLIQMDLPLVPGDKTHCDLILFAFTKNVLGSGGELDSLKTNMEEFM 1831
Qy 1693 EANPFKKLYEPIVITTKRKEEEOGAAVIQRAYRKHM 1728
Db 1832 ATNLSKASYEPIATLRKQEDLSNTVLOKAYRSYM 1867

RESULT 6

US-08-836-325-7
; Sequence 7, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Haleboua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2005 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-325-7

Query Match 48.8%; Score 4479.5; DB 3; Length 2005;
Best Local Similarity 48.18; Pred. No. 0;
Matches 950; Conservative 276; Mismatches 450; Indels 301; Gaps 38;
Qy 11 PDERNFRFTSDSLAAIKKRIAOK-----ERKSKDKAAAEQPPRQLDLKASRKLPK 64
Db 9 PGPDFRFTRESLAAIEORIAEAKKRPQERKDEDD-----ENGPKNSDLEAGKSLPF 64
Qy 65 LYGDIPPELVTKPLEDDPYKDKHTFMVLNKKRTIYRFSKAKRALFIIGPNPLSLMIR 124
Db 65 IYGDIPPELVTKPLEDDPYKDKHTFMVLNKKRTIYRFSKAKRALFIIGPNPLSLMIR 124
Qy 125 ISVHSVSMFTICTVIIINCMEFMANSMERSFNDIDPEYFVIGIYLEAVIKILARGFVDE 184
Db 125 ILVHSLFNVLIMCTILTNCFVMTSNPPDWTKNV-EYFTGIYTESLIKILARGFCLEDD 183
Qy 185 FSLRDPWNWLDIVIGTAIATCFPGSQVNLSALTRFVRFRALKAKAISVISGLKVIUGALL 244
Db 184 FTFLRNPWNWLDFTVITFAYVTEFV-NLGNVSALTRFVRFRALKAKAISVISGLKVIUGALL 242
Qy 245 RSVKKLVDVWVLTFLCLSFIFALVGOQLFMGILNKKCIKHNCGPNASN-----292
Db 243 QSVKKLSDVMILTVCFLSVFALIGLQLEFNGNLRNKLQW-----PPDNSTEEINITSPFN 297
Qy 293 -----KDCFEKEKDEDFIMCGTWLGSRRPCPNGSTCDKTT 327
Db 298 NSLDWNGTAFNRTVMNFMWDEYIEDKSHFYFLEGNDALLCGNSSDAQCPGEGYICVRAG 357
Qy 328 LNPNNTYKFNFGMSFLAMFRVMTQDSWERLYRILRTSGIYFVFFVWIFLGSFYLL 387
Db 358 RNPVGYTSPDTFSWAPLSLFRMLTQDFWENLYQLTLRAAGKTYMIFVFLVFLGSPYLI 417
Qy 388 NLTAIVTMAYEBEQNRNVAATEKAKMFQE-AQOLLREKEALVAM-----433
Db 418 NLILAIVAMAYEBEQNRNVAATEKAKMFQE-AQOLLREKEALVAM-----433
Qy 434 -GIDRSSLSLQASSFSFKKFKFGSKTRK-----462
Db 478 GGIGVFSESSVASKLSKSEKELKNRRKKKKQKQAGEEKEDAVRKSASEDSTRKKGF 537
Qy 463 SFMRGSKTAQ-----ASASDEDD-482
Db 538 QFSLGSLRITVEKRFSPHQSLLSIRGSLFSPRRNSRASLNFNFKGRVKDISENDFADDE 597
Qy 483 -----ASKNPOLLEQTKRLSONLPV-----502
Db 598 HSTFEDNDSRDSLFVPHRHGERRPSNVSQASRASRGITPLPMNGKMHSAVDCNGVSLV 657
Qy 503 -----DLFDE-----HV-----DPLHRORALSAVSILTIITQ 529
Db 658 GGPSALTSFVGQLLPGETTETEIRKRRSSSVHVSMDLLEDP-SQRAMSMASILTNTWE 716
Qy 530 EOEKQEPFCFPGKNLASKYLWDCSPQWLCKIKVLRITMDPTTELATITCIINTVFL 589
Db 717 ELESROKCPCCWKYKAFANCLIMDCCKPWLKVKHVNLVWMDPFDVLAITICIVLNTLFM 776
Qy 590 AVEHHNDDNLKTLIKIGNWVFTGIFIAEMCLKIITALDPYHYFRHGNVFDISVALLSLA 649
Db 777 AMEHPMTEQFSVSLVSGNLVFTGIFTAEMFLKIITANDPYTYFQEGWIFDGFIVLSLIM 836
Qy 650 DV-LYNTLSNDRSFLASLRVLFKAKSWPTLTNLTKIIGHSVGALGNLTAVLTIVVF 708
Db 837 ELGLANV---EGLSVLSRFLRLRVFKLAKSWPTLNLIKIIGNSVGLGNLTAVLTIVVF 893
Qy 709 IFSVGMRLFGTKFNKTAIATQ---ERPRRRHMDNFYHSFLVFRILCGEWIENWGM 765
Db 894 IFAVVGMQLFGKSKYKCVCKISNDCELP-RWHMHFFHSFLVFRVLCGEWETMWDGM 951
Qy 766 QDMGSPLCIIVFLIMVIGKLVNLNLIALLNLSFSNEKDGSGLEGTRTKVQALDR 825
Db 952 -EVAGQTMCLTVFMVMVIGLVNLNLIALLNLSFSNDNL-AATDDDDNMNLIQAVGR 1009
Qy 826 FRRAFSEFMLHALQSFCCCKKRRKNSP---KPKETTESFAGNKDSILDPARPWKEYDTD 881


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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-020B-4

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Query Match 47.9%; Score 4390.5; DB 3; Length 1988;
Best Local Similarity 47.2%; Pred. No. 0;
Matches 928; Conservative 290; Mismatches 469; Indels 281;

Qy	11	PDERNRPFTSDSLAAIKKRIATQKERRKSKOKAA-----AEQPPRPDLDKASRKLPKL	504
Db	9	PGDSEKPTTPESLANIERIAESKLKPKADGSHREDDDESKPKPNDSLEAGKSLPFI	505
Qy	66	YGDIPPELVTKPLEDDPYKYKHKTFWMLNKKRTIYFESAKRALFTILGPFENPLRSLUMIRI	506
Db	69	YGDIPQGLVAVPLEDDPPYLTOKTFVNLNRGKTLFFESNATPALYTLSPENLIRRAIKI	507
Qy	126	SVHSVFSMFICTVIINCMPMANSERSFNDIPEYVFIGIYILEAVIKILARGFIVDFE	508
Db	129	LIHSVFSMIITACTILNCVPMTESNPENSKNY-EYTFGTGYFESLWIKIIARGFCIDGF	509
Qy	186	SFLRDPNHWLDFVIGTAINTCPGSOVNLALSALTRPRVPALKAISVISGLKVIIVCALLR	510
Db	188	TFURDPNHWLDFEVIIMAYVTEF-DLGNVSALURTRFVRALKATISVIPGLKTIVIGALIO	511
Qy	246	SVKKLVDVWLTLFCLSFIFALVGQQLFMGLNCKIKHNGCPNA-----	512
Db	247	SVKKLSVMIITVFCLSVFALIGLQFMGNLRNKCVMVPINFNFSYLENCTRCGFDWEEYI	513
Qy	291	SNKDCPEKEDSEDFMCGTWLASRCPNGSTCKDTLPLNDNNYTKFDNFGWSFLAMFRV	514
Db	307	NNKTNFTVYVPMLEPLLCGNSDAGQCPEGFQCMKAGRPNYGYTSFDTFSWAFALFRL	515
Qy	351	MTQDSWERLRYOILRTSGIYVFVFVVYIFLGSFYLLNLTLLVVTWAYEONRNVAATE	516
Db	367	MTQDYWENLQTLRLRACKTYMIFVLVIFVGSFYLVNLILAVVAKAYEQNQRTLEBAE	517
Qy	411	AKEMFQOE-AQOLLREPEKEALVA-----MGIDRSSNLSLQASSF	518
Db	427	QKEAEFKAMLEQLKKQOEBAQAAMATTSAGTIVSEDAIEEBEGDGVGSPRSSSELSKSK	519
Qy	449	SPKKR-----KFGSKT-----RKSEFM-----	520
Db	487	SAKERNRNRKKRQKELSEGEKGDPEKVPKSESDGMRRKAFRLPDNRIGRKFSIMNOS	521
Qy	467	-----RGSKTAQASADSE--DDASKN-----	522
Db	547	LLSTPGSPFLSRHNSKSSIFSRGPRFDPGSENEFADDEHSTVESECGRDSLFIPR	523
Qy	487	-----POLLEOTKR-----LSQNLIPVDL	524
Db	607	ARERRSSYSGYSQCSRSRIFPSPSLRRSVKRNSTVDCNGVVSILGPGSHIGRLLPEVK	525
Qy	505	FDE-----HVDPL-----HQRALSAVSILTIH-IQOEKRFQEP	526
Db	667	IDKAOTSATTEVEIKKKGCSLLVSDMQLASTYGRKDRINSVVTNLVEEESQRK	527
Qy	538	CFPGCKNLASKYLVMDGSPOWLCKIKVLRITMDPTETELAITIICIINTVFLAVEHHMD	528
Db	727	CPCCWYKAFNTLWECHPYWIKLEIVNLVMDPPFDLAITICIVLNTLFMAHEHPMT	529
Qy	598	DNLTKILIGNWVFTGIFIAEMCLKIALDPYHYFRHGNVNFSDISVALLSLADLVNTYLS	530
Db	787	PQFEHLVLAUGNLFTGIFTAEMLFKIAMDPPYFYFOEGWNIPDGFIVISLSMBL---SLA	531
Qy	658	D-NNRSFSLASLRVRFKLAKSNPTLNTLKIIGHSVGALGNLTVTLTVTFVFSVVGMR	532
Db	844	DVEGLSVLRSFRLRLRVFKLAKSNPTLNLKILIGNSVGALGNLTVLAIIVFIFAVVGMQ	533
Qy	717	LFCTKFNK-TAYATQPRRRRHMDNFYHSFLVYVFRILCGEWTIENWGCMDMGSGPLCI	534

RESULT 9
US-08-836-325-11

Qy 1134 RALSOFGKVVVALISAIPAILNVLVCLIFWLVFCILGNVLSFGKGRCTDINM 1193
Db 1299 RALSRFEGMRVVALIGAISIMNVLVCLIFWLVFCILGNVLSFGKGRCTDINM 1358
Qy 1194 YLDTVEPNRSOC---NIS-NYSKVPQVNFNDVGNAYLALLOVATYKGLWLEINRAVD 1248
Db 1359 F-PXSQVNRSECFALMNVSNVNRKNNLVNFDNVLGVLQVATFKGWXIMYAAVD 1417
Qy 1249 SREDEQPDFEANYLVYFVFIIFSFFTLNLFVIGVINDFNQOQKKGQDIFMTEE 1308
Db 1418 SVNXQPKYEYSLYMYFYXKFIIFSFFTLNLFVIGVINDFNQOQKKGQDIFMTEE 1477
Qy 1309 QKKYNNAMKLGTKKPKQPIPRPLNKQAFVDFVLSQVDFVILGLIVLNMIMMAESA 1368
Db 1478 QKKYNNAMKLGSKPKQPIPRPGNKQCGIFDLVTNOAFDIXIMVILCLNMTMWEKE 1537
Qy 1369 DQPKDVKTDFILNFAVFIETIECLIKVAFALROHYFTNGWNLFDVGVVLSIIST-LVS 1427
Db 1538 QXXXXXVLXWIXNVFIILFTGCVLKLISLRHYFTVGNWIXXVGVVIXSIVGMFLAX 1597
Qy 1428 RLEDSISFPPTLFRVRLARIGRILRLVRAARGIRTLILFALMMSLPSLNFILGLLFLVM 1487
Db 1598 XIENYFVS--PTLFRVRLARIGRILRLXKCAKIGRTLLFALMMSLPALENLGLLFLVM 1655
Qy 1488 FIYAIFGNSWFSKVKSGGIDIFENFTFTGSMCLCFOITTSAGWDTLINPMLEA----- 1542
Db 1656 FIYAIFGNSFAYKKGXGINDFNFTFGNSMICLFOITTSAGWDGLLAPILNXPDP 1715
Qy 1543 ---KEHCNSSQDSQOQOIAVVFVSVIIISFLIVNMVYIAVILENNTATESESDPLG 1599
Db 1716 DPKVHPGSSVGGCGNPSGVIFVSVIIISFLIVNMVYIAVILENFSVATESESTPLS 1775
Qy 1600 EDDFEIFYWEKEDPEASQFIQXSALSDFADALPEPLRVAKPNKQFVLVMDLPMVMGDR 1659
Db 1776 EDDFEIFYWEKEDPDATQFIEXKLSDFAAALDPLLIAPKPKVOLIANDLPVSGDR 1835
Qy 1660 LHCDVLPFAFTRVLGDSGLDWTWKTMMEEKFMEANPKLYEPIVTTTKRKEEQGA 1719
Db 1836 IHCLDILFAFTRVLGEXGENDSLRSQMEERFMSANPSKVSYPEITTTTLKRKQXVSATX 1895
Qy 1720 IORAYRKHMEKWLRLKDRSSS 1743
Db 1896 IORAYRRI-----RLRQXVKNISS 1914

RESULT 10
US-09-024-020B-9
; Sequence 9, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024, 020B
; FILING DATE: 16-FEB-1998

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1976 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
OS-09-024-020B-9

Query Match 47.1% Score 4316.5; DB 3; Length 1976;
Best Local Similarity 46.8% Pred No. 0;
Matches 915; Conservative 293; Mismatches 478; Indels 269; Gaps 37;

Qy 11 PDERNFRPTSDSLAAIKKRIAIQERKKSKDKAA-----AEPQPRPOLDLKASKRLPKL 65
Db 11 PGPSDFKPTPELANIERRIAESKLLKPPKADGSHREDDEDSKPKPNSDLEAGKSLPFI 70
Qy 66 YGDIPELVTPLEDDPYKDKHTFVNLKRTYRFSAKRALFILGPNPLSLMRI 125
Db 71 YGDIPELVTPLEDDPYKDKHTFVNLKRTYRFSAKRALFILGPNPLSLMRI 130
Qy 126 SVHSVFSFICTVILNOMENANSMERSFDNDIPEYVIGYILEAVIKILARGFVDF 185
Db 131 LIHSVFSFICTVILNOMENANSMERSFDNDIPEYVIGYILEAVIKILARGFVDF 189
Qy 186 SFLDPNWNLDVIFVIGTAIATCFPGSQVNLALRTFRVFRALKATISVGLKIVIGALLR 245
Db 190 TFLDPNWNLDVIFVIGTAIATCFPGSQVNLALRTFRVFRALKATISVGLKIVIGALLR 248
Qy 246 SVKLLVDMVITLFCLSIFALVGQOLFPMGILNKCINCKINCPNPA----- 290
Db 249 SVKLLVDMVITLFCLSIFALVGQOLFPMGILNKCINCKINCPNPA----- 308
Qy 291 SNKDCFEKEKDESEFILMGTLGSRPCPGSTCDKTTLPDNNYTKFDNFGMSFLAMFRV 350
Db 309 NKNTFNVMVPMLEPLICGNSSDAGQC--EGFQCCKAGRNPNYGYTSFDTFSWAFIALPRL 367
Qy 351 MTQDSWERYLRQILRTSGIYFVFFVIFLGSFYLLNLTLAVVTMYEEOGNRVAAATE 410
Db 368 MTQDYWENLYQILTRAGKTYMIFVLVIFVGSFYVNLILAVVAMAYEEOGNQATLEAE 427
Qy 411 AKEMFOE-AOOLREKEALVA-----MGIDRSSUNLSQASSF 448
Db 428 QKEAEFKAMLEQLKQOEAEQAAAMATSGATVSEDAIEEGEDGVGSPRSSSELSKLSK 487
Qy 449 SPKKR-----KFFGSKT-----RKSF----- 464
Db 488 SAKERNRKRKRKOKELSEGEKEGDPKVFKESEYGMRRKAFRLPDNRIGRKFSSIMNQS 547
Qy 465 -----FMRGSKTAQASASDSE--DD----- 482
Db 548 LLSIPGSPFLSRHNSKSSIFSGDPSPDRDPCSENEFADDEHSTVEESEGRDLSLPIRA 607
Qy 483 -----ASKNPOLLEQTKRLSONLPVD-----LFDEHVD 510
Db 608 RERRSSSYGSGYSCSRSSRISPAQAQREANSTVDCNGVSVSLIGSGHIGRLLRQLR 667
Qy 511 PLHRQALSAVSILIT-----IQOEKFOEPFCPGKNLASKYL 550
Db 668 WKLRRKALDSFSGYPTLRLLRTEGONQOHNHGRGHKHAEELEESQKPCPCWYKPAFTFL 727

Qy 551 VDCSPQWLCKIKVLRITMDPTTELAIITCIITVFLAVEHHMDDNLTILKIGNV 610
Db 728 IWECHPYWIKULKEIVNLVMDPFVDLAITICIVLNTLFEMAEHPMTQPFHVLAIGNLV 787
Qy 611 FTGFIAMCKLIATLADPDYHYFRGNWVDSIVALLSLADVLYNTLSD--NNRSFLASLURV 669
Db 788 FTGFIAMCKLIATLADPDYHYFRGNWVDSIVALLSLADVLYNTLSD--NNRSFLASLURV 844
Qy 670 LRVEFLAKSWPTLNTLKIIGHSGALCNLTIVLTIVVIFSVVGMRLFCGPKNK--TAY 728
Db 845 LRVEFLAKSWPTLNTLKIIGHSGALCNLTIVLTIVVIFSVVGMRLFCGPKNK--TAY 904
Qy 729 TOERPRRWHMDFHSLFVFRILCGEWIENMGCMQMDGSLPCIIVFVLMVIGKLV 788
Db 905 NOECKLPRWHMDFHSLFVFRILCGEWIETMDCM--EVAGOAMCLIVPMWVIGNLV 963
Qy 789 VLNFIALLNSFNE-----EKDGSLEGETRKTQVOLALDRFRRAFSEMLHALQSCCK 843
Db 964 VLNFIALLNSFNE-----EKDGSLEGETRKTQVOLALDRFRRAFSEMLHALQSCCK 1017
Qy 844 KCRKNPKKETTSEFAGENKDSILP-----DARPKKEYTDMALYTGQAGAPLAPLAE 898
Db 1018 HFKORADEVPLDEL--Y--ERKANCIAHNTGVDIHRNGDFQKNGTTSIGGVSVEKYII 1075
Qy 899 VEDDVEYCGGALPTSQHSAGVQAGDLPETKQLTSPDQGVEMEFSEEDLHLSQSP 958
Db 1076 DEHMSFINN---PNTLVTRVPIAVE--SDFENLTED-----VSSSED-----PEGS 1118
Qy 959 RKSDAVMSLSECTIDLNDIFRNLQKTVSPKO-----PDRCFPKGLSCHFFCHTKDK 1012
Db 1119 KDKLDDTSS--SEGSTIDIKPEVEV-----PVEQPEYLDPDACFTGECVQRKCCQVNI 1172
Qy 1013 RKSFWLWNNIRKCYOIVKHWSFESFIIVILLSSGALFEDVNLPSRPOVEKLLRCTD 1072
Db 1173 EEGUGKSWILURKCYOIVKHWSFESFIIVILLSSGALFEDVNLPSRPOVEKLLRCTD 1232
Qy 1073 NIIFTIFELLEMILKWAFGRFRYTSACWCLDFLIIVVSVLSL-----NLPKLSKFR 1125
Db 1233 KVFTYIFILEMLLKWTFYGFVKFFTNACWCLDFLIIVVSVLSL-----NLPKLSKFR 1292
Qy 1126 TLRALPLRALSQEGKVVVYALISAIPAILLVLLVCLIFWLFCILGNVLFSGKGRG 1185
Db 1293 TLRALPLRALSQEGKVVVYALISAIPAILLVLLVCLIFWLFCILGNVLFSGKGRG 1352
Qy 1186 INGT--DINMYLDTEFVNRSC-----NISNSYKVPQVNDVGNAYLALLOVANYKG 1238
Db 1353 FNETSEIRFEDI--VNKTDCEKLMGNSTEIRKNNKYNFNDVNGAGYLLALQVATFKG 1410
Qy 1239 WLEINNAVDSRDEQDPFEANLYAYLYFVVFIFIGSFFTLNLFIGVIIDNFNQOKKL 1298
Db 1411 WMDIMYAAVDSRDEQDPFEANLYAYLYFVVFIFIGSFFTLNLFIGVIIDNFNQOKKL 1470
Qy 1299 GGQDIFWTEGOKKYNNAMKLGTKPKOKPPIRPLNKKOAFVDFDLVTSQVDFVILGLIVL 1358
Db 1471 GGQDIFWTEGOKKYNNAMKLGTKPKOKPPIRPLNKKOAFVDFDLVTSQVDFVILGLIVL 1530
Qy 1359 NMIMMAESADQPKDKVTFDILNIAFWLFTIECLIKVVALROHYETNGWNLFDVVVV 1418
Db 1531 NMIMMAESADQPKDKVTFDILNIAFWLFTIECLIKVVALROHYETNGWNLFDVVVV 1590
Qy 1419 LSIIST--LVSRLESDISFPPTLFRVVRVLARIGRILRLVRAARGIRTLFLFALMMSPLSF 1477
Db 1591 LSIIST--LVSRLESDISFPPTLFRVVRVLARIGRILRLVRAARGIRTLFLFALMMSPLSF 1648
Qy 1478 NIGLLFLVFIYAFGMSWFSKVKSGGIDDIENFTFTGSMCLCFQITTSAGWDPLLN 1537
Db 1649 NIGLLFLVFIYAFGMSWFSKVKSGGIDDIENFTFTGSMCLCFQITTSAGWDPLLN 1708
Qy 1538 PMLEA-----KEHCNSSSDQSQOQOIAVYVYVYIIISFLVIVNMYIAVILENNTA 1590
Db 1709 PILNRPDCSLDKHPSGSGKDCNCSVGIFFVSVIIISFLVIVNMYIAVILENNTA 1768
Qy 1591 TEESDPLGEDDDFEIFYVWEKFDPEASQFTQYSALSDFADALPEPLRVAKPNKQFLVM 1650

Db 1769 TEESADPLSEDDFEIFYVWEKFDPEASQFTQYSALSDFADALPEPLRVAKPNKQFLVM 1828
Qy 1651 DLPVMDGRHLCMDVLAFTTRVLGDSGLDTMTKMMEEKMEANPFFKLYEPIVTTTKR 1710
Db 1829 DLPVMDGRHLCMDVLAFTTRVLGDSGLDTMTKMMEEKMEANPFFKLYEPIVTTTKR 1888
Qy 1711 KEEBGAAGVIAQRAYRKHM-----EKWKLRLKD 1738
Db 1889 NEEVSAVVUORAYRGLARRGFCIRKMASNKLEN 1923
RESULT 11
US-08-836-325-15
Sequence 15, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Haleboua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Usi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-15
Query Match 45.6%; Score 4185; DB 3; Length 1835;
Best Local Similarity 48.9%; Pred. No. 0;
Matches 939; Conservative 266; Mismatches 397; Indels 320; Gaps 64;
Qy 11 PDERNFRPFTSDSLAAIKKRIAIQKRRKSKDKAAAEPPQRPQLDLKASRLPKLYGDIP 70

Db 7 PPGQSFVFTKQSLALIQR--IEKKEKKD-----DEEPPSSDLEAGKOLPFIYGDIP 60
Qy 71 PELVTKPLEDDPYKDKHRTFVNLKRTIYRFSAKRALFILGPFNPLSMIRISVHSV 130
Db 61 PGMVSEPLEDDPYVADKKTIVLNKKG-IFRENATPALYMLSPFSLRISIKILVHSL 119
Qy 131 FPMIICITVINCMFMANMERSFNDNPIPEVFGIYILEAVIKILARGFIVDESFURD 190
Db 120 FSLIMCTILTNCFMTNP---PMTKNV--YTFGTIYTFES-LKILARGFCVGEFTLR 173
Qy 191 PWNMLDFTVICTATJATCFPGSOVNLRSALRTRFRALKAIISVIGLKVIVGALLRSVKKL 250
Db 174 PWNMLDFVIVFAYLITEV-NLGNVSALRTRFRVLRALKATISVIPCLKTIVGALIQSVKKL 232
Qy 251 VDMVLTILFCLISIFALYGOQLFMGLNOKCIKHNGCP-----NPAASNKDCFEKEKSDSF 305
Db 233 SDVMILTIVFCLSVFALIGLQFMGLNKHKCFRLENETLESIMTSEBEKYFYLEGSKDA 292
Qy 306 IWCWTGLGSRPCPNGSTCDKTLTPDNNYTKFDNFGHVSFLAMFRVMTODSWERYLQILR 365
Db 293 LLCGFSTDSGQCPEG-YCVKGR-NPDGYGTSFDTFSWAFALFRMLTQDYWENLYQOPLR 350
Qy 366 TSGIVFVFVFFVFLGFSYLLNLTLAVVTMAYEEONRNVAATEAKEMFQEAQQLLR- 424
Db 351 AAGKTYHILFFVFLGFSYLLNLTLAVVAMAYEEONQANIEBAKQKLEFQOQLDRUKK 410
Qy 425 --EKEALVA-----MGIDRSLNSLOASSFSPPKRRKFFGSK----- 459
Db 411 EOEAEALAAAAAETSIRSIRIMGLSESS-SETSLSSKSAKERRNRKQKQKSSKEEGD 469
Qy 460 -----TKRSFPM-----RGSKTA-----Q 473
Db 470 EKLKSSSESIRKSFHLGVEHREKRLSTPNQSPLSIRGSLFSARRSRTSLFSFKGRGD 529
Qy 474 ASASDEDD-----ASKNP----- 487
Db 530 GSETEFADDEHSIFGDNESRRGSLFVPHRPERRSNISQASRPPLPVNGKMHSAVDCNG 589
Qy 488 -----QLLEQ-----TKRLSONLPVDLDFEHVDPLHQRALSAVSLITITI 528
Db 590 VVSLVDSGSLMLPNCOLLPEGTNOKRSSLSEMDLN--DPL-RQRAMSRASILITV 645
Qy 529 QEQEKFPQPCPKGNKSLASKYLWDCSPQWICIKKVLRTIMPTPELAIITICIIINPVF 588
Db 646 BELBESROKY-----RPAHELWNCSPLYWIKKKIYFIVM-DPEVDLAIITICIVNLTF 699
Qy 589 LAVEHHNDDNLKTLIKIGNVFTGIFIAEMCLKIIALDPHYRPHGHNVFDSIVALLS- 647
Db 700 NAMEHHPMTBEEKNVL-AGN-LFTGIFAAEMVLKLIAMDPEYFQVGNIFDSLIVTSL 757
Qy 648 ---LADVLYNTLSDNNRSLASRLVRFKLAKSWPTLNTLKIIGHSVGALGNLTVVLT 704
Db 758 ELFLADV-----EGLSVLSRFLRLRVFKLAKSWPTLNTLKIIGHSVGALGNLTIVLA 810
Qy 705 IWTFISVVMRLFGTKFNKATAYAQE-RPRRRHMDNFHYSFLVFRILCGEWIENMWG 763
Db 811 IIVFIFAVVGMOLFCKSKYKCVCKINDCLP--RWHMNDFFHSLFVFRVLCGEMIETMWD 868
Qy 764 CMQMDGSPCLIIIVFLVLMVGLKVLWNLFTALLNFSNEEKDGLSLEGTRTKVQVAL 823
Db 869 CME--VAGOMCLIVMYMVVGNLVNLFLALLSLSSFSNLTAAIEEDDANNLQIAVRI 926
Qy 824 DRFRRAFSLHALQFQCKCRKRNKSPKKT--TESFAGENKDSILDPARPWKYD-- 879
Db 927 ----KGINYVQTLREFILFKSKPKSDNKKENYISNTLAEMSKHNL-----KERDIS 976
Qy 880 -----TDMALYTQAGAPLAPLAEVEDDVEYCGEGALPTSOHSAGVQAGDLPPETKOL 933
Db 977 GGSSDKMDOSFIHNPSTLTVTVPIAPGESDLEM-----NEEL 1012
Qy 934 TSPDQGVEMEVFSEEDLHLSIQSPRKSDAVSMLSEGSTIDLNDIFRNLOKTVSPKQP 993

Db 1013 SSDSD-----SYSKNRSS-----SEGSTVDNPLPGEGEAEAEAPNDP 1051
Qy 994 DRCPKGLSCHFLCH-KTKRKSPWLVWNNIRKTCYQIVKHSWFESFIFIVILLSSGALI 1052
Db 1052 EACFTDGCVRRCOVNSGKCK---WM-IRKTCY-IVEHSWFESFIVILLSSGALA 1104
Qy 1053 FEDVNLRSRPOVEKLLRCTDNIFTFIFLLEMLKWAAGFRFRYFTSANCWLDLFLVVVS 1112
Db 1105 FEDIYI-EKTKIKILEYADKIFTYIFILEMLLKW-AYGYKTYETNAMCWLDLFLVDVSL 1162
Qy 1113 LSLM-----NPLSLKSFRLRALRPLRALSQFEGKMKVYVALISATIPALINLVLLCLI 1165
Db 1163 VTLVANTLGYSDLGPIKSLRTRLRALRPLRALSREFGHRVYVVALIGALIPSTMNVLVCLI 1222
Qy 1166 FWLVCILGVNLFGKFGRCINGTDINMYLDFTEVPNRSQC-----NISNYSWKVPQVNF 1221
Db 1223 FWLIFSIMGVNLFAKGYEC-NTTDGSR---FPQVNRSECFALMNVSNVRWKNLKVNF 1278
Qy 1222 NVGNAYLALLOVATYKGLHLEIMNAAYDSREKDEQDPEANLYAYLYFVVFIFGSEFTLN 1281
Db 1279 NVGLGYLSLLQVATFKG--IMYAAVDS--VNVQPKYEYSYMYIYF-VFTIFGSEFTLN 1333
Qy 1282 LFIVGIIDFNNOQOKKLGQDIFEMTEOKKYNNAMKLGTKPKPKPIPRPLNKQOAFYD 1341
Db 1334 LFIVGIIDFNNOQOKKLGQDIFEMTEOKKYNNAMKLGSKKPKPKPIPRPNK-QGCIFD 1392
Qy 1342 LVTQVEDVITLGLVILNMIIMAESADQPKDKVKTFTDILNI-APVVIITIECLIKVPAL 1400
Db 1393 L-TNOAFDIIV-LICLNMVTMVEKEGQ-----VLWINVFIILFTGECVLKLISL 1442
Qy 1401 RQHFETNGWNLDFCVVVLVLSIISTLVSRLESDISFPPTLFRVVRVLARIGRILRLVRA 1460
Db 1443 RHYFTVGVNIF---VVVISIVGMFLA---IEYFVSPTLFRVIRLARIGRILRL-KGAK 1494
Qy 1461 GIRTLLPALMSLPSLNFNIGLLFLVMFIYALFGMSWFSKVKKSGIDDIENFETGSM 1520
Db 1495 GIRTLLPALMSLPSLNFNIGLLFLVMFIYALFGMSWFSKVKKSGIDDIENFETGSM 1553
Qy 1521 LCLFQITTSAGMDTLLNPMLEA-----KEHCNSSQSDSCQOQIAVIVFVSYIIISFL 1573
Db 1554 ICLFQITTSAGMDGLLAPILNSPPCDPKVHPGSGVEGDCGNPSVGIFVSYIIISFL 1613
Qy 1574 IVWNYIAVILENNTATESEDEPLGEDDFEIFYEVWEKFPDEASQFTQYSAISDFADAL 1633
Db 1614 VVWNYIAVILENVSATESEDEPLSEDDFEMFVWEKFPDQATQFTEFK-LSDFAAAL 1672
Qy 1634 PEPLVAKPNKFOELVMDLPMVMDRLHCDVLFATFTRVLGDSGLDTMTMMEKEPME 1693
Db 1673 DPPLLIAKPNKVQLIAMDLPVSGDRIHCLDILFAFTKRVLGEGE-MDSLRSQMEERPMS 1731
Qy 1694 ANPKKLYEPIVTTTKRKEEBQGAIVQIARVKKHMEKVK-----LRLKDRSSSHOVF 1747
Db 1732 ANPSKVSYEPIITLKRQEV--SATIQARVRLRQVKNLISSIIYIKGDRDDDLNKNDF 1789
Qy 1748 CN 1749
Db 1790 DN 1791

RESULT 12

US-08-808-793-3

Sequence 3, Application US/08808793

Patent No. 5858713

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.

APPLICANT: Ingles, Patricia J.

TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

Db 1524 MYLVFFIIFGSEFTLNLFVIGIDNFEQKKAGSLEMFTEQOKKYNAKMGSK 1583
Qy 1323 KQKPIPRPLNKKCAFVDFVLTQVDFVILGLVLNMIIMAESADQPKVKKTFDILN 1382
Db 1584 KPLKAIPRWRPQAIIVEIVTDKFDIIMFLGCLNNFTWLDYDASEAYNNVLKLN 1643
Qy 1383 IAFVVIETIECLIKVAFALROHYFTNGWNLDCVWVVISIITLVSRL-LESDISFPPTLF 1441
Db 1644 GIFVIFSGECLLIKAFALRVHYFKEPNWLFVWVVISLGLVLSDIIEKYFVS--PTLL 1701
Qy 1442 RVVRLARIGRLRLVRAARGTIRTLFALMNSLPSLFNIGLILFLVMIYIIFGHSWFSKV 1501
Db 1702 RVWRAVGRVRLVKGAKGIRTLFALMSLPALFNICLLFLVMIYIIFGHSFMHV 1761
Qy 1502 KKGSGIDIFNFETFTGSMCLCFQITTSAGWDTLLNPMLEAKEHCNSSOD-----SCQQ 1556
Db 1762 KEGSGINAVNFKTFGSMILLFOMSTAGWDGVLDAIIN-EEDCDPPDNCKGYPGNGS 1820
Qy 1557 PQIAVTVFVYIIISFLIVNMYIAVILENNTATESEDPGLGEDDFEIFYVWEKFDPE 1616
Db 1821 ATVGITELLSVLISFLIVNMYIAVILENYSOATEDVQEGLTDDYDMYIEIWOQFDPE 1880
Qy 1617 ASQFIQSALSDFADALPEPLRVAKPNKQFLVMDLPMVWCDRLHCHMDVLFATFTRVLGD 1676
Db 1881 GTQVIRYDQSEFLDVLEPPLOIHKPNKTIISMDNPTCRGDMYICVDILDALTKDFFAR 1940
Qy 1677 SSGLDTKMMEKFEANPEKPIEPIVTTTKRKEEEOGAAVTORAKH 1727
Db 1941 KG--NPITEGEIGEIAARPDTEGDPVSSTLWRQREYCAKLIONAWRRY 1989

RESULT 13
US-08-772-512A-3
; Sequence 3, Application US/08772512A
; Patent No. 6022705
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Knipple, Douglas C.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
; TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,512A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,618
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Branan, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/601(CRFD-1657)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2105 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-772-512A-3
Query Match 38.7%; Score 3554.5; DB 3; Length 2105;
% Best Local Similarity 38.4%; Pred. No. 0;
Matches 780; Conservative 357; Mismatches 533; Indels 361; Gaps 39;
Qy 9 IFPPERN-FRPFTSDSLAAKKRIATIAQKERRKKSKDKAAAE-----PQRPQ 53
Db 8 ISEERSLFRTRESLQTEQRIAEHEKQERKRAAGEQIRYDEDEDEQPDPT 67
Qy 54 LDKASKKLPP---KLYGDIPPELVTKPLELDLPYVKDQKTPMVLNKKRTIYRFSAKRALF 110
Db 68 LE-----OGVPVPMQCSFPPELASTPLEDIDPFYSNVLTFVVISKGDIFRFSKAMW 123
Qy 111 ILGPNFLRLSIRISVHVSFMFICTIIVINCMMANSMERSFDNDPIEYFVIGIYLE 170
Db 124 LLDPENPTRRVAIVILVHPLFSLEFIITILNLCILMI--MPTTPTVESTVEITGVTFE 181
Qy 171 AVIKILARGFIVDEFSLRDPNWLDFIVIGTATATCFPGSQV--NLSALRTFRVFRALKA 229
Db 182 SAVKVMARGFTLCPFTYLRDANNWLDVFVIALAYVTM--GIDLGNLAAALRTFRVLRALK 239
Qy 230 ISVTSGLKIVGALLRSVKLVDMVLTFLCLSFALVGQOLPMGLNOKCIK----- 282
Db 240 VAVPGLKTVGAVIESVKNLROVLIITMFSLSFALMGLOIYMGVLTQKCIKRPDLGS 299
Qy 283 -----HNGCPNPASNKDCFEKEKSEDFIMCGTWTGSRPCPNGSTC-DKTTINP 330
Db 300 WGNLTDENWFLHN-----SNSSNWFTENDGESYPCGVNSVSGACGEDYVLOGFGPNP 353
Qy 331 DNNYTKDFNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYVFFVVFVIFLGSYLLMLT 390
Db 354 NYDYTSDFSFGWAFLSAFLMTQDFWEDLYQHVLAQAAGPHMLFFIIFLGSFVLNLI 413
Qy 391 LAVVTMAVEQNRVNAATEAKEKMFQEAQOLL----- 423
Db 414 LAIVMSYDELOKKAEEEAEEBAIREAEEAAKAAKLEERANVAQAQAADAAAA 473
Qy 424 -----REEKEALVAMGIDRSSN----- 441
Db 474 ALHPEMAKSPYISCIYSYELFVGEGKNDNKNKMSIRSVESESVIQRQAPTAP 533
Qy 442 -----SLQASSFSPPK-----RKFFG--SKTRKSFPMRGSKTAQA 474
Db 534 ATKVRKVSTTSLSLPGSPFNLRGSRSSHKYTIRNGRGRFGIPGSDRKLVLQTYDQAQ 593
Qy 475 SASDSEDDASKNPQ----- 488
Db 594 HLPYADDSNAVTPMSENGAIIVPAYCNLGRSHRSYTSYSHOSRISYTSYSHGDLGMAAMG 653
Qy 489 ---LLEQTKRLSON-----IQEQKFOEPCPCGKNLASKYL 550
Db 714 HHDNPFIEPVQTVVDMKDVMLNDITEQAAGRHSRASEGEDDEDGPTFKDIALEYI 773
Qy 551 -----VWDCSPWLCIKKVLKTIIMTDPETELATITCIILNTVFLAVEHHNDDNLT 602
Db 774 LKGEIFCWDCWCCWVWLKFQEWVSFIVDPPEVELFICIVNTMFMAMDHMDNPELEK 833
Qy 603 ILKIGNVFTGIFTAEMCKITIALDPVHYFRHGNWVDSIVALLSLADLVNTLSNNRS 662
Db 834 VLKSGNYFFATFAIEASMKLMSPKYYFQEGNWFEDFIIVALSLLLELGEV--QGLS 891
Qy 663 FLASLRVLRVFKLAKSWPTLNTLTKIIGHSVGALGNLTIVVTFISVVGMLFGTKF 722
Db 722 FLASLRVLRVFKLAKSWPTLNTLTKIIGHSVGALGNLTIVVTFISVVGMLFGTKF 722

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 26, 2002, 22:49:55 ; Search time 72.7 Seconds
(without alignments)
1849.355 Million cell updates/sec

Title: US-09-646-224A-2
Perfect score: 9173
Sequence: 1 MEERYYPVIFPDNERFRPFT.....VFCNGDLSLDVAKVKVHND 1765
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9157	99.8	1765	2 T42388	sodium channel alp
2	4724	51.5	2019	2 A33996	sodium channel pro
3	4711	51.4	2016	2 A38195	sodium channel pro
4	4553	49.6	1977	2 S34771	sodium channel alp
5	4545	49.6	1957	2 S68453	sodium channel pro
6	4501	49.1	2005	2 A46269	sodium channel alp
7	4496	49.0	1951	2 S00320	sodium channel pro
8	4489	48.9	1983	2 A60054	sodium channel pro
9	4484	48.9	2005	2 B25019	sodium channel pro
10	4476	48.8	2009	2 A25019	sodium channel pro
11	4363	47.6	1840	1 CHRTM1	sodium channel pro
12	4355	47.5	1836	2 I64893	sodium channel alp
13	4347	47.4	1836	2 I51964	sodium channel alp
14	4342	47.3	1836	2 J50648	sodium channel alp
15	4331	47.2	1835	2 I54323	sodium channel alp
16	4316	47.1	1976	2 I36555	sodium channel pro
17	3983	43.4	1820	1 CHEE	sodium channel pro
18	3518	42.7	2049	2 T43161	sodium channel pro
19	3554	38.7	2108	2 S72458	sodium channel pro
20	3512	38.3	1784	2 T43167	sodium channel pro
21	3479	37.9	1993	2 T30902	sodium channel SCA
22	3242	35.3	1820	2 A33299	sodium channel pro
23	3184	34.7	1682	2 A45380	sodium channel pro
24	3032	33.1	1689	2 S72467	sodium channel pro
25	3021	32.9	1681	2 A55138	sodium channel mRNA
26	3016	32.9	1699	2 T31340	voltage-gated sodi
27	2959	32.3	1810	2 T31092	probable voltage-g
28	2945	32.1	1522	2 JC1101	sodium channel pro
29	2732	29.8	1321	2 A60165	sodium channel pro

ALIGNMENTS

RESULT 1

T42388

sodium channel alpha chain - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T42388

R:Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.

Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998

A:Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in perip

A:Reference number: 222149; MUID:98338024

A:Accession: T42388

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1765 <DTB>

A:Cross-references: EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC40199.1

A:Experimental source: strain Sprague-Dawley; dorsal root ganglia

A>Note: preferentially expressed in sensory neurons within dorsal root ganglia and t

C:Superfamily: sodium channel protein

Query Match 99.8%; Score 9157; DB 2; Length 1765;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1761; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEERYYPVIFPDNERFRPFTSDSLAAIKKRIAIQKERRKSKDKAAAEOPRQOLDLKASR 60

Db 1 MEERYYPVIFPDNERFRPFTSDSLAAIEKRIAIQKERRKSKDKAAAEOPRQOLDLKASR 60

QY 61 KLPLKLYGDIIPPELVTKPLEDLDPYKDKHTFMVLNKKRTIYRFSAKRALFILGPNPLRS 120

Db 61 KLPLKLYGDIIPPELVAKPLEDLDPFYKDKHTFMVLNKKRTIYRFSAKRALFILGPNPLRS 120

QY 121 LMRISVSHVSFMFTICTVIINCMFMANSMERSFNDIPEYVFIGIYILEAVIKILARGF 180

Db 121 LMRISVSHVSFMFTICTVIINCMFMANSMERSFNDIPEYVFIGIYILEAVIKILARGF 180

QY 181 IVDESFRLDPNWLDFIVIGTAIATCPGSOVNLISALRTFVRFKALKAISVISGLKIV 240

Db 181 IVDESFRLDPNWLDFIVIGTAIATCPGSOVNLISALRTFVRFKALKAISVISGLKIV 240

QY 241 GALLRSVKLVDMVMTLFLCLSFALVGQQLFMGLINQKCIKHNGCPNPASNKDCFEK 300

Db 241 GALLRSVKLVDMVMTLFLCLSFALVGQQLFMGLINQKCIKHNGCPNPASNKDCFEK 300

QY 301 DSEDFIMCGTWTGSRPCPNKSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERY 360

Db 301 DSEDFIMCGTWTGSRPCPNKSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERY 360

QY 361 RQILRTSGIYFYFFVFWVIFLGSFYLLNLTAVVTMAYEQNRNVAATEAKEMFQEAQ 420

Db 361 RQILRTSGIYFYFFVFWVIFLGSFYLLNLTAVVTMAYEQNRNVAATEAKEMFQEAQ 420

QY 421 QLLREEKALVAMGIDRSLNSLQASFSFKRRKFFGSKTRKSFMRGSKTAQASADSE 480
DB 421 QLLREEKALVAMGIDRSLNSLQASFSFKRRKFFGSKTRKSFMRGSKTAQASADSE 480
QY 481 DDAKNPQLLEQTKRLSNLQVLDLDEHVDPLHQRALSAVSLITITOEQEKFOEPCFP 540
DB 481 DDAKNPQLLEQTKRLSNLQVLDLDEHVDPLHQRALSAVSLITITOEQEKFOEPCFP 540
QY 541 CGKNLASKYLVDWCSPQWLCIKKVLRTITWDPFTELATITICIIINTVFLAVEHHNMDNL 600
DB 541 CGKNLASKYLVDWCSPQWLCIKKVLRTITWDPFTELATITICIIINTVFLAVEHHNMDNL 600
QY 601 KTLKIGNVFTGIFIAEMCKLIATLDPYHFRHGNVFNDSIVALLSLADLVNLTLSNN 660
DB 601 KTLKIGNVFTGIFIAEMCKLIATLDPYHFRHGNVFNDSIVALLSLADLVNLTLSNN 660
QY 661 RSFLASRLVRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFISVGMRLPCT 720
DB 661 RSFLASRLVRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFISVGMRLPCT 720
QY 721 KFNKTAYATQERPRRWHNDNFYHSFLVVFRLCGEWENMGCMQDMGSPCLCIIVFVL 780
DB 721 KFNKTAYATQERPRRWHNDNFYHSFLVVFRLCGEWENMGCMQDMGSPCLCIIVFVL 780
QY 781 IWIIGKLVVNLFIALLNSFSNEEKDGLSEGETRKTQVQALDRFRRAFSFMLHALQSF 840
DB 781 IWIIGKLVVNLFIALLNSFSNEEKDGLSEGETRKTQVQALDRFRRAFSFMLHALQSF 840
QY 841 CCKKRRKNSPKPKETTESFAGENKDSILDPARPNKEYDTDMALYTGQAGAPLAPLAEVE 900
DB 841 CCKKRRKNSPKPKETTESFAGENKDSILDPARPNKEYDTDMALYTGQAGAPLAPLAEVE 900
QY 901 DDVEYCGEGGALPTQSHSAGVQAGDLPETTKQLTSPDQGVMEVFSEEDLHLSQSPRK 960
DB 901 DDVEYCGEGGALPTQSHSAGVQAGDLPETTKQLTSPDQGVMEVFSEEDLHLSQSPRK 960
QY 961 KSDAVSMLSECTIDLNIFRNLOKTVSPKQDPDRCPFKGLSCHFLCHTKDKRKSPPWLW 1020
DB 961 KSDAVSMLSECTIDLNIFRNLOKTVSPKQDPDRCPFKGLSCHFLCHTKDKRKSPPWLW 1020
QY 1021 WNIRKTCYQVVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIPTFIFL 1080
DB 1021 WNIRKTCYQVVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIPTFIFL 1080
QY 1081 LEMILUKWAFGRFRFTSAWCHLDPLIVVSVLSLNMNLPKLSKSFTRLALPLRALSQFE 1140
DB 1081 LEMILUKWAFGRFRFTSAWCHLDPLIVVSVLSLNMNLPKLSKSFTRLALPLRALSQFE 1140
QY 1141 GMKVYVYALISAIPAILNVLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTFV 1200
DB 1141 GMKVYVYALISAIPAILNVLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTFV 1200
QY 1201 PNRSCNITSNYSWKVPQVNFQVNGVAYLALQVATYKGLWLETMNAAVDSREKDEQDPFEA 1260
DB 1201 PNRSCNITSNYSWKVPQVNFQVNGVAYLALQVATYKGLWLETMNAAVDSREKDEQDPFEA 1260
QY 1261 NLAYLYEVVFLIGSFETLNLFGVIIDNENQOQKLGCGDIFMTEQKKYNNAMKLG 1320
DB 1261 NLAYLYEVVFLIGSFETLNLFGVIIDNENQOQKLGCGDIFMTEQKKYNNAMKLG 1320
QY 1321 TKKPKQPIRPLNKOAFVFDLVTSQVFDVITLGLVNLNMIIMAESADQPKDKVKTEDI 1380
DB 1321 TKKPKQPIRPLNKOAFVFDLVTSQVFDVITLGLVNLNMIIMAESADQPKDKVKTEDI 1380
QY 1381 LNIAPVFTIECLIKVPALRQHYFTNGWNLFDVGVVVLVLSIISTILVSRLESDISFPPTL 1440
DB 1381 LNIAPVFTIECLIKVPALRQHYFTNGWNLFDVGVVVLVLSIISTILVSRLESDISFPPTL 1440
QY 1441 FRVVLARIGRLRLVRAARGIRTLFLFALMMSLPSLFNIGLILLFLVMFIYAFGNWFSK 1500
DB 1441 FRVVLARIGRLRLVRAARGIRTLFLFALMMSLPSLFNIGLILLFLVMFIYAFGNWFSK 1500
QY 1501 VKGSGIDDIFNFETFTGSMCLCFQITTSAGWDTLNPNMPEAKEHCNSSQSCQOPIA 1560

DB 1501 VKGSGIDDIFNFETFTGSMCLCFQITTSAGWDTLNPNMPEAKEHCNSSQSCQOPIA 1560
QY 1561 VYFVSYIIISFLIVVNMVIAVILENFNTATSESDPLGEDDFEIFYEWEKFDPEASQF 1620
DB 1561 VYFVSYIIISFLIVVNMVIAVILENFNTATSESDPLGEDDFEIFYEWEKFDPEASQF 1620
QY 1621 IOYSALSDFADALPEPLRVAKPNKFOQLVMDLPMVMDLPHCMVDLFAFTTTRVLGDSSGL 1680
DB 1621 IOYSALSDFADALPEPLRVAKPNKFOQLVMDLPMVMDLPHCMVDLFAFTTTRVLGDSSGL 1680
QY 1681 DTMKTMMEKFEANPEPKLYEPIVTTTKRKEEGEAAVIOYRAYRKHKMKVYKRLKDRS 1740
DB 1681 DTMKTMMEKFEANPEPKLYEPIVTTTKRKEEGEAAVIOYRAYRKHKMKVYKRLKDRS 1740
QY 1741 SSSHQVFCNGDLSSLDVAKVKVHND 1765
DB 1741 SSSHQVFCNGDLSSLDVAKVKVHND 1765
RESULT 2
A33996
sodium channel protein I, cardiac - rat
N:Alternate names: sodium channel protein (SkM2) alpha chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 20-Aug-1999
C:Accession: A33996; JQ0412
R:Rogart, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8170-8174, 1989
A:Title: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) chan-
A:Reference number: A33996; MUID:90046760
A:Accession: A33996
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2019 <RG>
A:Cross-references: GB:M27902; NID:g206857; PIDN:AAA42114.1; PID:g206858
R:Kallen, R.G.; Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.
Neuron 4, 233-242, 1990
A:Title: Primary structure and expression of a sodium channel characteristic of dene-
A:Reference number: JQ0412; MUID:90166613
A:Accession: JQ0412
A:Molecule type: mRNA
A:Residues: 1-479, 481-1712, 'T', 1714-1963, 'R', 1965-2019 <KAL>
A:Experimental source: muscle
C:Superfamily: sodium channel protein
C:Keywords: cardiac muscle; duplication; heart; sodium channel; transmembrane protei-

Query Match 51.5%; Score 4724; DB 2; Length 2019;

Best Local Similarity 50.2%; Pred. No. 0;

Matches 976; Conservative 284; Mismatches 426; Indels 260; Gaps 32;

QY 15 NRPFTSDSLAAIKRIAIOKER-----KSKDKAAAEPPRPOLDLKASRKLKLYGD 68

DB 12 SFRRTRESLAIEKRAEQAQGSATSQESREGLEEEAPRPOLDLQASKLPDLKYN 71

QY 69 IPPELVTPLEDDLPYKDKHTFVNLNKKRTIYRSKRALPILGPPNPLRLMIRSVH 128

DB 72 PPRELIGPELDDLPYSTQKTFIVLNKGKTIRESATNALVLSPPFPVRAAAKILVH 131

QY 129 SVFSMFICTVIINCMFANSMERSFDNDIP-----EVVFTGIVILEAVIKILARGFTV 182

DB 132 SLFSMLINCTIITNCFVNA-----QHDPPPTWYVEYTTTATYTFESLVKILARGCL 184

QY 183 DEFSFLRDPWNWLDIFVIGTATATCFPGSQVNLRSALTRFRFRALKAISVISGLKVIYA 242

DB 185 HAFTFLRDPWNWLDIFSVIVMAYTTTEFV-DLGNVSALTRFRVLRAKLTIVISGLATIVA 243

QY 243 LLRSVKLVVDVNLVTLFCLSFALVQQLFMGILNQKIKINC-----GNPASNKD----- 294

DB 244 LIQSVKKLADYVNLVTLFCLSVFALVGLQFLMGNLRRHKVRNFTLEUNGTSVEADGLVWN 303

QY 295 -----CFEKEKDEDFIMCTGTLGSRPCPNSTGCTKTTLNPDNNYTKFDNFGWSF 344

Db 304 SLDVYLDNPANYLLKNGTDTVLLCGNSSDAGTCPEGYECLKAGENPDHGYTSFDSFAWAF 363
Qy 345 LAMRVMTQDWERLYROILRTSGTYVFFVFWVIFLGSFYLLNLTLLAVTWMAYEEQNRN 404
Db 364 LALFRLMTQDWERLYQOTLSAGKIYIMFIMLVIFLGSFYLVNLIILAVAMAYEEQNOA 423
Qy 405 VAAETEAKKWFQEAQQLLREKEALVANGIDRSSLSLQASFSF-----KKRFF 456
Db 424 TIAETEKKRFQEAEMLEKHEALTIIRGVDTVSRSSLEMSPLAVTNHERKSKRRRL 483
Qy 457 GSKT-----RKSFMRGSKTA-----QASASD 478
Db 484 SSGTEGDDRLPKSDSDGPRALNQLSLTHCLSRMTPRPSRSGSIFTRRRDQGSAD 543
Qy 479 SEDASK----- 485
Db 544 FADDENSTAGSESHRTSLLVPWPLRHPSAQGPQPGASAGYVNLNGRNSVTDCNGVVS 603
Qy 486 -----NPQLEQ-----TKRLSONLP-VDLFEDEHVDPLHR 514
Db 604 LLGAGDAEATSPGYSLLRPMVLDLPPDTPPTSEPPGGPQMLTPQAPCADGFE-----PGAR 660
Qy 515 ORALSAYSILTTIOEQEKFOEPCPCGNLASKYLWDCSPQWLCIKKVLRTIMTDPT 574
Db 661 ORALSAYSILTSALTEEESHRKPCPCWNRFAQHYLIWECCPLMWSIKQKVKFVMDPFA 720
Qy 575 ELATITCIIINTVFLAVHHNDDNLTKIKIGNVFTGIFTAEACLKIIIALDPVHYPRH 634
Db 721 DLTITMCIVLNTLPMALHYNNTAEFEMLQVGNLVFTGIFTAEAKTFKIIIALDPVHYFQ 780
Qy 635 GWNVDSIVALLSADVLNTLSNNRSLASRLVRFLKAKSWPTLNTLIKIGHSVG 694
Db 781 GWNVDSIVALLSMEGLSRM--GNLSVLSRFLRLVRFLKAKSWPTLNTLIKIGHSVG 838
Qy 695 ALGNLTVLTIVVLESVVGRLGCTKFNKATAYATOER---PRRWHMDNYHSLVYFR 751
Db 839 ALGNLTVLTIVVLESVVGRLGCTKFNKATAYATOER---PRRWHMDNYHSLVYFR 896
Qy 752 ILCGEWENMGCMQDMGSLPCLIVFLIMVIGKLVNLFIALLLNSFSNE-----EK 806
Db 897 ILCGEWENMGCMQDMGSLPCLIVFLIMVIGKLVNLFIALLLNSFSNE-----EK 860
Qy 807 DGSLEGETRKYQLALDRFRRAFSLMHLAQSCCKCKRRK----- 848
Db 956 DGEM-----NNLQALARIQGLRFVKKRTTWDFCCGLRRLRRPKPAALATHSOLPSCIT 1009
Qy 849 --NSPKPKETTESFAGENKDSILPDARPKWEYDIDMALYTQAG--APL-APLAEVEDDV 903
Db 1010 APRSPPPPEVEK-----VPPARKETFEEDKRPQGGTGPDSPEVCVPIAAESDT 1059
Qy 904 EYCGE-----GGALPTSOHSAGVOAGDLP-----ETKQLTSPDQGVEMEVFSEE 949
Db 1060 EDQEDENSLGTTEESKQESQVVSQGHPEYQPRAWSQVSETTSSAGASTSQADWQ 1119
Qy 950 DLHLSIOSPRKKSDAVSMLSECSITDLN---DIFRNLQKTVSPKQDRCPPKGLSCHFL 1006
Db 1120 EQKTEPQAGCGETPDSYSGSTADMTNTADLLEQIPDLGEDVKDPCDETCGVCRRCP 1179
Qy 1007 CHKTDKRSKPVWLNIRKTCQIVKHSWPFESFIIFVILLSSGALIFEDVNLPSRPQVEK 1066
Db 1180 CCMVDTTQSPQKVMRLRKTCYRIVEHSWFETFIIFMLLLSSGALAFEDIYLERKTKIV 1239
Qy 1067 LLRCTDNLTFTIFLLEMLTKWAFGRFRTYSAWCVLDLFIWVSVLSLM-----NLP 1119
Db 1240 LLEVADKFTVTVVLEMLLKWAVGFKYFTNACWDLDFLVDVLSLVANTMTLGFADM 1299
Qy 1120 SLKSFTLRALRPLRALSQFGEMKVVYVALISAIPAILNVLVLCILFVLCILGVNLF 1179
Db 1300 PIKSLRTLALRPLRALSREFEMRVVYVALGAIPIINVLVLCILFVLCILGVNLF 1359
Qy 1180 KFGRCINGTIDNMYLDETEVPNRSQCNISY-----WKVPQVNFNDVGNVAYLALQVAT 1235
Db 1180 KFGRCINGTIDNMYLDETEVPNRSQCNISY-----WKVPQVNFNDVGNVAYLALQVAT 1235

Db 1360 KFGRCINGTIDNMYLDETEVPNRSQCNISY-----WKVPQVNFNDVGNVAYLALQVAT 1419
Qy 1236 YKGLMEINAAVDSREKDEQDFEALYLYFVVFVFIIFGFFTLNLFIVGIDNFNOQ 1295
Db 1420 FKGWMDINAAVDSRGVEEQWEDNLYYFVVFVFIIFGFFTLNLFIVGIDNFNOQ 1479
Qy 1296 KKLGGDIFMTTEBOKKYNNAMKLGTKKPKQIPRPLNKCAQAFVFDLVTSQVDFVILGL 1355
Db 1480 KKLGGDIFMTTEBOKKYNNAMKLGSKKPKQIPRPLNKYQGFIDIVTKOAFDVIMFL 1539
Qy 1356 IVLNMIIMMAESAQDPKDKKTFDILNIAFVVFVFIIECLIKVFALRQHYFNGHLPDV 1415
Db 1540 ICLNMVTMMVETDDOSPEKVNILAKINLLFVAIFTEGECIVKMAALRHHYFTNSWNIFDV 1599
Qy 1416 VVLSIISTLSRLSDSDISFPPTLFRVRLARIGRILRLVRAARGIRTLFLFALMMSLPS 1475
Db 1600 VVLSIVGTVLSLIIQK-YFESPTLFRVRLARIGRILRLIRGAKGIRTLFLFALMMSLPA 1658
Qy 1476 LFNIGLLFLVNFYIAFGMSWFSKVKGGSDIDFENFTFTGSMCLCFQITTSAGWDTL 1535
Db 1659 LFNIGLLFLVNFYISFGMANFAYVKWEAGIDDMFNQTFEANSMLCLFQITTSAGWDTL 1718
Qy 1536 LNPML-AKEHC-----NSSQSDSCQOPIAVVYFVSYYIIISFLIVNMVIAVLENFN 1588
Db 1719 LSPILNTPPYCDPNLPSNGSRGNCSPAVGILFTTIIISFLIVNMVIAVLENFN 1778
Qy 1589 TATESEDPGLGDDFEIYEVWEKFPDPEASQFIQYALSADADALPEPLRVAKPNKFOFL 1648
Db 1779 VATESEDPGLGDDFEIYEVWEKFPDPEASQFIQYALSADADALPEPLRVAKPNKFOFL 1838
Qy 1649 VMDLPMVMDRLHCHMDVLFATFTRVGLDSSGLDTMKTMEKFMFANPKLYEPIVTT 1708
Db 1839 NMDLPMVMDRLHCHMDVLFATFTRVGLDSSGLDGMKALQMEKFMFANPKLYEPIVTT 1898
Qy 1709 KRKEEEOCAAVIOARVKKH-MEKVVK 1733
Db 1899 RKKEEVSATVIQAFRRHLQORSVK 1924
RESULT 3
A38195
sodium channel protein hHI, cardiac - human
N:Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-1
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: A38195
R:Gellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barchi, R.L.;
Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A:Title: Primary structure and functional expression of the human cardiac tetrodotoxin
R:Reference number: A38195; MUID:92115699
A:Accession: A38195
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-2016 <GEL>
R:Cross-references: GB:M77235; NID:g184038; PIDN:AAA58644.1; PID:g184039
R:Experimental source: heart
R:Superfamily: sodium channel protein
C:Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium

Query Match 51.4%; Score 4711.5; DB 2; Length 2016;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 970; Conservative 281; Mismatches 435; Indels 247; Gaps 29;

Qy 15 NFRFTSLSAAIKKRIATQKER-----KSKDKAAAEQPPQDLKASRLKPKLYGDI 69
Db 12 SFRRFTRESLAIEKMAEKAQSGSTTLQESREGLEPEAPRPQDLQASKKLPDLYGNP 71
Qy 70 PPELVTKPLEDLDVYKDKHTFMVNLKRTIYRESAKRALFLLGPNLRLMIRISVHS 129
Db 72 POELIGEPELDLDVYKDKHTFMVNLKRTIYRESAKRALFLLGPNLRLMIRISVHS 131
Qy 130 VFSMFICTIINCMMANSERSFDNDIP-----EYVFIGIYLEAVIKILARGFIVD 183

A:Molecule type: mRNA
A:Residues: 1-1957 <AKO>
A:Cross-references: GB:X92184; MID:g1209466; PIDN:CAA63095.1; PID:g1209467
A:Experimental source: Gorial root ganglia
C:Superfamily: sodium channel protein
C:Keywords: sodium channel; transmembrane protein; voltage-gated ion channel
F:132-148/Domain: transmembrane #status predicted <TM1>
F:158-174/Domain: transmembrane #status predicted <TM2>
F:225-241/Domain: transmembrane #status predicted <TM3>
F:249-265/Domain: transmembrane #status predicted <TM4>
F:376-392/Domain: transmembrane #status predicted <TM5>
F:666-682/Domain: transmembrane #status predicted <TM6>
F:702-718/Domain: transmembrane #status predicted <TM7>
F:731-747/Domain: transmembrane #status predicted <TM8>
F:788-804/Domain: transmembrane #status predicted <TM9>
F:865-881/Domain: transmembrane #status predicted <TM10>
F:1156-1172/Domain: transmembrane #status predicted <TM11>
F:1194-1210/Domain: transmembrane #status predicted <TM12>
F:1221-1237/Domain: transmembrane #status predicted <TM13>
F:1286-1302/Domain: transmembrane #status predicted <TM14>
F:1400-1416/Domain: transmembrane #status predicted <TM15>
F:1482-1498/Domain: transmembrane #status predicted <TM16>
F:1516-1532/Domain: transmembrane #status predicted <TM17>
F:1546-1562/Domain: transmembrane #status predicted <TM18>
F:1606-1622/Domain: transmembrane #status predicted <TM19>
F:1708-1724/Domain: transmembrane #status predicted <TM20>

Query Match 49.6%; Score 4545.5; DB 2; Length 1957;
Best Local Similarity 51.0%; Pred. No. 0;
Matches 966; Conservative 265; Mismatches 446; Indels 217; Gaps 36;

QY 15 NFRPFTSDSLAAIKRIAIQERKSKDKAAAE-----PQRPOLDKASRLPKLYGDIP 70
DB 12 NFRFTPSLEAEIEQIAHRAAKARKYHRGQDEKGRPOLDKDCNQLPKRYGELP 71

QY 71 PELVTKPLEDDPYVKDKHTFVNLNKRRTIYRFSAKRALFLTGLPPNPLRLSIRLSVHSV 130
DB 72 AELVGEPLDLPFYSTHRTFVNLNKRRTISRFSATWALWLFSPNPLRRTAIVKSVHSW 131

QY 131 FSMFTICVINCMPANSMERSFNDIP-----DLPEKVEYVFTYITFEALIKILARGFCLEFTEY 184
DB 132 FSIFITITILNVCVCMRT-----DLPEKVEYVFTYITFEALIKILARGFCLEFTEY 184

QY 188 LRDPNNWLDVIGTAITACFPGSOVNL-----SALRTFRVFRALKAISVISGLKVIIVGALL 244
DB 185 LRDPNNWLDVITLIA-----YVGAIDLRLGISGLTFRVLRALKTVSVIPGLKVIIVGALI 240

QY 245 RSVKLVDMVWLTLFCLSFALVGQOLFPMILNQKCIKNCNPNPASKDCFEK-----299
DB 241 HSVRLADWTLITVPCLSVFALVGLQFKGNLKNKCIKNCNPNPASKDCFEK-----299

QY 300 KDSDFIMCGTWLGRPCPNGSTCDKTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWRL 359
DB 301 PGTDPDLCCGNSDAGHCPGGVCLKTPDNPFDNYTSPDSFAWFLSLFRMTQDSWRL 360

QY 360 YRQILRTSGIVFVFPFVIFLGSYLLNLTLAVVTMAEYEQNRNVAAETAEKAKMFOEA 419
DB 361 YQOTLRASGKMYVFFVILFGLSYLLNLTLAVVTMAEYEQNRNVAAETAEKAKMFOEA 420

QY 420 QQLREKEALVAMGIDRSSLSNLSQASSFSP-----KKRKFSGS-----458
DB 421 LEVLQKEQVLEALGIDITSLQSHSGSPLASKNANERPVRKSRVSEGSTDDNRSQSDP 480

QY 459 --KTRKSFPMGSGTKTAQASD-----SEDDA-----483
DB 481 YNORMSPLGLSGRRASRSHSVFHRAPSQDISFPDGIPTDGGVFHGDQESRRGSILLG 540

QY 484 -----SKNP-----QLLEQTKRLSONLP-----VDL 504
DB 541 RGAGTGPLRSPPLPQSPNRRRGEQGLGVPTGELTAGAPALHTTQOKSFLSAGY 600

QY 505 FDEHVDPLHRORALS AVSILITITIQEQEKFOEPFCPCGNLASKYLVWDCSPQWLICKV 564

DB 601 LNE-----PRAQRAMSVSVMTSVIEELDESKLCPCLISFAQKLYLWECCPKWRKFKMA 657
QY 565 LRTIMTDPTELAITICIIINTVFVLAVERHNNMDDNLTKITLIGNVWVFTGIFTAEMLCKII 624
DB 658 LFEVTDPAELTITLCIIVNTVFVMAHYPMTDAFQDLQAGNIVETVFTMEMAFKII 717
QY 625 ALDPYHYFRHGNVFDISVALLSLADVLYLNTLSDNNRSLASLRLVRFKLAWSPTLNT 684
DB 718 APDPYHYFQKWNIFDCVITVTSLEL--SASKKGSLSVLRLLRLRFLKLAWSPTLNT 775
QY 685 LIKIIGHSVAGALNLTIVVTFVIFSVVGMRLFGTKF--NKTAYATQBRPRRRHMDNF 742
DB 776 LIKIIGSVGALNLTIFLAIIVFIFALVKGKLLSEDCYCRKDGVSVMNGEKLRRHMDCF 835
QY 743 YHSFLVFRILCGEWIENMGMQMDGSPGLIIVFVIMVIGKLVNLNLFALLNSFS 802
DB 836 FHSFLVFRILCGEWIENMGMQMDGSPGLIIVFVIMVIGKLVNLNLFALLNSFS 894
QY 803 NE-----EKDGSLEGETRKTQVQLALDRFRRAFSFMLHALQSFCCCKCR-----RKNS 850
DB 895 ADNLTAPEDDGEV-----NNQLALARIQVGLHGRASRAIASYISSHCRFHWPKVETQLG 948
QY 851 PKPKETTESFAGENKDSILPDA-----RP-----WKEDYTDMLTYTGQAGAPL 893
DB 949 MKPPLT-----SSEAKNHATDAVSAVGNLTYPALSSPKENHGDFITDENVW---VSVP 1001

QY 894 A-----PLAEVEDDVEYC-----GEGALPTSQHSAGVAGDLPPTKQLTSPDD 938
DB 1002 AEGESDLDLEDEDMEOASQSSWOEDPKGOQBOLPOVKCNHQHAARSP--ASMSSEDL 1059

QY 939 QGVNEVSEEDHLISQSPKKSDAVSMSECSIDLND---IFRNLOKTVSPKKQDPR 995
DB 1060 APYLGESWRRKD---SPOVPAEGVDDTSS--SEGSTVDCPDPEILRKIPELADDDLEPDD 1115

QY 996 CFPKLSGCHFLCHTKDRKSPVLMWNIRKTCYQVVKHSWFSEFIFIVILLSSGALIFED 1055
DB 1116 CFTEGCTRRCCPCNVNTSKSPWATCQVRYKVEHSWFSEFIFIVILLSSGALAFED 1175

QY 1056 VNLSPRPOVEKLLRCTDNIFIFLLEMLKWAAGFRYRFTSACWDLDFLIVVSVLSL 1115
DB 1176 NYLEKPRVKSLEYLTDVFTFIFVEMLLKWAYGFKYFTNACWDLDFLIVVSVLSL 1235

QY 1116 M-----NLPSLKFRTLRALRPLRALSOPGEMKVVVVALISAPAILNVLVLCIPLW 1168
DB 1236 TAKILEYSDVASIKALRTRALRPLRALSOPGEMKVVVVALISAPAILNVLVLCIPLW 1295

QY 1169 VFCILGVNLSGKFGRCINGTDINMY--LDTEVEPNRSCNIN---YSWKVPQVNFEN 1222
DB 1296 LFSIMGVNLSGKFGRCINGTDINMY--LDTEVEPNRSCNIN---YSWKVPQVNFEN 1354

QY 1223 VGNAYLALQVATYKGLWEIMNAADVDSREKDEQDQPEANLAYLYFVFIPIGSPFTLNL 1282
DB 1355 VAMGYLALQVATEKGMWDIMYAAVDSGEINSQPNWENNLYMYLYFVFIPIGSPFTLNL 1414

QY 1283 FIGVIIDNFNQOKKLGQDIFMTEEQKYYNAMKLGTKPKQKPIPRPLNKCQAFVPL 1342
DB 1415 FVGVIIDNFNQOKKLGQDIFMTEEQKYYNAMKLGTKPKQKPIPRPLNKCQAFVPL 1474

QY 1343 VTSQVDFVIIILGLIIVLNMIMMAESADQPKVKTFTDILNIAFVFIPIECLIKVFLARQ 1402
DB 1475 VTRQAFDIIIMVILCLNMTMMVETDEGEKTKVLGRINOFFVAVFTGECVKKRFAALRQ 1534

QY 1403 HYFTNGWNLPCVVVVLISITLVSRL--LEDSDISFPPTLFRVVRILARIGRLRLVRAARG 1461
DB 1535 VYFTNGWNVDFVIVILSIGSLFSAILKLSLENYFSPFLFRVIRLARIGRLRLVRAARG 1594

QY 1462 IRTLLFALMMSLPSLFNIGLLLLFLVMFYIAFGMSWFSKVGSGIDIDIFNFTGSM 1521
DB 1595 IRTLLFALMMSLPSLFNIGLLLLFLVMFYIAFGMSWFSKVGSGIDIDIFNFTGSM 1654

QY 1522 CLFQIWTTSAGWDTLLNPMLE-AKEHC-----NSSQSDSCOOPOIATVYFVSYIIISFLI 1574
DB 1574 CLFQIWTTSAGWDTLLNPMLE-AKEHC-----NSSQSDSCOOPOIATVYFVSYIIISFLI 1574

QY	436	DRSSLNSLOASFSFKKKRFFGSGKTRKS	-----FF	465
		: :		
Db	481	GVFSESSVASKLSKSEKELNRRKKKKQEQSGEEKNDRVLKSESDSIRKKGRFPS	540	
		:		
QY	466	MRCGSKT-----AQASASD	478	
		:		
Db	541	LEGSRLTYEKFSSPHQSLLSRGSLFSPRRNSRASLFSGRAKDIGSENDADFDPHST	600	
		:		
QY	479	SEDDASKNPQL-----LEOTKRLSONLPV-----	502	
		:	:	
Db	601	FEDNDSRRSLFVPHRHGRRHSNVQSASRASRLPILPMNGKMHSVDCNGVVSLVGGP	660	
		:		
QY	503	-----DLFDE-----HV-----DPLHRRORALSVAVSILTITIOBOEK	533	

[illegible]

Qy	830	FSFALHALUSFCUKCRKRANS	---KRAETTESFAGENKUSILFDPARFKNEIDIMALI	8895
Db	1014	IDFVKRKIRIEFTQAKAFVRKQKALDEIKPLEDINN	---KKDSCISN	1055
Qy	886	TGQAGAPLAPLAEVEDDVEYCEG	---GALPTSQHSAGVQAGD---LPPETKQLTSP	936
Db	1056	-----HTTTEIGKDLNLYKDGNGTSG	TGSSVEKYKVDSEYMFNNPSLTVTVPI	1107
Qy	937	-----DQGVMEVESEEDLHLSIQSPRK	KDAVSMLSECTIDLNDIFRLQKTVSPKK	991
Db	1108	AVGESDFENLNTSEFSSES	---DMEESKEKLNATSS-SEGSTDVIGAPAGEQVEPEEP	1163
Qy	992	--OPDRCPFKGLSCHFLCHHTDKRSPVW	MWNIRKTCYQIVKUSHWESFTIIFVILLSSG	1049
Db	1164	SLEPEACFTEDCVKRFKCCQISIEBEGK	KLWNLNKRCTCYKIVEHNWFTFTFVPMILLSSG	1223
Qy	1050	ALIFEDVNLPSPOVEKLLRCTDNLTFT	FEILEMLLKWVAFGRYRTSASWCWLDFLIV	1109
Db	1224	ALAFEDITYEQRKTITMILEYADKVFTY	IFILEMLLKWVAFGOVFTNACWLDFLIVD	1283
Qy	1110	VSVLSL-----MNDPSLKSFTLRAL	RLPRLALSOFGMKVWYVALISAIPALINLVV	1162
Db	1284	VSLVSLANALGYSELGAKTSURTLAR	LPRLALSRPEGMRAVYNALLGAIPSTMNVLLV	1343
Qy	1163	CLIFLWFLCILGNLFSGRGKRCINGTDIN	MYLDTFVPNRSOCNI---SNYS--WKVPQ	1217
Db	1344	CLIFLWLFISMGVNLFAGRFYHCIN	YTTGEMF-DVSVVNNYSECKALIESQOTARKNVK	1402
Qy	1218	VNFDNVGNAYLALLQVATYKGMLET	MNNAVDSREKDEQDPDEANLYAYLVFVPIIFGFS	1277
Db	1403	VNFDNVGLGYLSLLQVATEFKGWM	DMYAAVDSRNVELQPKYEDNLWYLVFVPIIFGFS	1462
Qy	1278	FTLNLFIGVLIIDNFQOQKLLGGODI	FWTEEOKKYYNAMKKLGTCKKQKPTIPRPLNKCQA	1337
Db	1463	FTLNLFIGVLIIDNFQOQKLLGGODI	FWTEEOKKYYNAMKKLGSKKKQKPTIPRPNKFOG	1522

QY 1205 QCNI--SNYSKVKVPOVNFNVGNVAYLALLOVATYKGMLEIMNAAVDSREKDEQDPFANL 1262
D 1334 DCQALGQARKNKVNFVNDVNGAGYALLQVATEKFGWMDIMYAAVDSRDVKLQPIYEENL 1393
QY 1263 YAYLVFVFIIFGFFFLNLFVIGVVIDNFNOQOKKLGQDIFWTEBQKYYNAMKKLGTK 1322
D 1394 YMYLVFVFIIFGFFFLNLFVIGVVIDNFNOQOKKFGQDIFWTEBQKYYNAMKKLGSK 1453
QY 1323 KPOKPIRPLNKKQAFVLDVTSQFVVIILGLVLNMIIMMAESADQPKDKKTFDILN 1382
D 1454 KPOKPIRPAKFGQVDFVTVROVFDISIMILCLNKNVMAVETDDQSKVMTLVLSRIN 1513
QY 1383 IAFVVFIEICLVKFAALROHYFTNGWNLFCVNVVVISIISTLVSRLEDSIDISPPPTLF 1441
D 1514 LVFVLTGTEPLKLLISLRVYVFTGNWIFDVVVVILSVGMFLAELIEKYFVS-PTLF 1571
QY 1442 RVVRLARIGRLRLVRAARGTIRTLFALMMSLPSLFNIGLGLLVLMYIYAFEGMSWFSV 1501
D 1572 RVIRLARIGRLRLVRAARGTIRTLFALMMSLPSLFNIGLGLLVLMYIYAFEGMSWFSV 1631
QY 1502 KKGSGIDDIFNFETFGSMCLFOITTSAGWDTLLNPMLEAKE-----HCNSSSDS 1553
D 1632 KKEAGIDDMFNFTFGSMCLFOITTSAGWDTLLNPMLEAKE-----HCNSSSDS 1601
QY 1554 CQPOIAVYVSVYIIISFLVNMVYIAVILENFNTATESESDPLGEDDFEIFYEWEKF 1613
D 1692 CGNPSVGIFVSVYIIISFLVNMVYIAVILENFNTATESESDPLGEDDFEIFYEWEKF 1751
QY 1614 DPEASQIOTYSALSDADALPEPLRVAKPNKQFLVMDLPVMDGRHLCHMDVLAFTTRV 1673
D 1752 DPDAOTIEFCKLSLDAADPPLLIAKPNKVLIAMDLPVMDGRHLCHMDVLAFTTRV 1811
QY 1674 LGDSGLDTMTKMEKFMENPKKLYEPTVTTTKKEEBOGAIVTORAKHMEKMYK 1733
D 1812 LGESGEMDALRIQWEDFMASNPVSEYPTITTLKRRQEVSAIITQRYCY---LLK 1868
QY 1734 LRLKDRSS 1741
D 1869 ORLKNISS 1876
RESULT 8
A60054
sodium channel protein IIIB, long form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C:Accession: A60054; B4824
R:John, R.H.; Moorman, J.R.; VanDongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster, Brain Res. Mol. Brain Res. 7, 105-113, 1990
A:Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in Xe
A:Reference number: A60054; MUID:90251117
A:Accession: A60054
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1983 <SOH>
R:Schaller, K.L.; Kremen, D.M.; McKenna, N.M.; Caldwell, J.H.
J. Neurosci. 12, 1370-1381, 1992
A:Title: Alternatively spliced sodium channel transcripts in brain and muscle.
A:Reference number: A4824; MUID:92211397
A:Accession: B4824
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 611-662 <SCH>
A:Cross-references: GB:597388; NID:9248225; PIDN:AAB21984.1; PID:9248226
A:Experimental source: skeletal muscle
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: sodium channel protein
C:keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane protein

Best Local Similarity 48.5%; Pred. No. 0;
Matches 951; Conservative 283; Mismatches 436; Indels 291; Gaps 38;
QY 11 PDENRERPTSDSLAAIKRTAIOKERRKSKDK-AAAEQPPRPOLDLKASKRLKVLXGDI 69
D 9 PGPESFRLFTRESLAAIEKRAAEKAKPKKEQDIDDKPKPKNSDLSEAGANLFTFYGI 68
QY 70 PPELVTPLELDPPYKDKHTFMVNLNKRRTIYRESAKRALFILGPFNPLRLMIRISVHS 129
D 69 PPEVSEPLELDPPYVSKTKTFVVLNKGKAFRESATSALVILTPNPKVRIAKILVHS 128
QY 130 VFSFIICTVIINCFMANSERSEFDNDIPEYFIGIYILEAVIKILARGFIVDEFSLR 189
D 129 LFSMLIMCTIITNCFVMTLSNPPDWTKNV-EYTFGIYITFESLILKILARGCLEDFTFLR 187
QY 190 DPWNLDFIVIGTAIATCFPGSQVNLASALRTFRVFRALKALSIVISGLKVIYVALLRSVKK 249
D 188 DPWNLDFIVIGTAIATCFPGSQVNLASALRTFRVFRALKALSIVISGLKVIYVALLRSVKK 246
QY 250 LVDVMTLTLCLSFALVQQLFMGLNKCICKHNCGPNASNKDCFEKEDS----- 302
D 247 LSDVMTLTLCLSFALVQQLFMGLNKCICKHNCGPNASNKDCFEKEDS----- 300
QY 303 -----EDFIMCTWLGSRPCPNMGSTCDKTTLNPD 331
D 301 SNGTFVNVMTSTFNWKDYIADDSHFYVLDGQKDLPLCCGSDAGOCPEGYICVKAQRPN 360
QY 332 NNYTKDFNFGSFLAMERVTQDSWERLYROILRTSGIYFVFFVWVIFLGSFYLLNLTL 391
D 361 YGYTSEDTFSAFLUSLFLMTQDYWENDYQTLRAAGTKYIMFVFLVIFLGSFYLLNLTL 420
QY 392 AVVTMAYEEQNRAAATEAKEKMFQEAQALLREEKALVAN-----GT----- 435
D 421 AVVAMAYEEQNRAAATEAKEKMFQEAQALLREEKALVAN-----GT----- 435
QY 436 -----DR----- 437
D 481 LLESSEASKLSKSAKEWNRNRKRQREHLEGNRADGDRFPKSESDSVKRRSFLLS 540
QY 438 -----SSLNSLOASSFSPPKKR-----KFFGSKT----- 460
D 541 LDGNPLTGDKKLCSPHOSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGESEDFADDEHST 600
QY 461 -----RKSPFM-----RGSKTAQASAD-----SEDDASKNPQLLBQ 493
D 601 FEDSESRDLSLFPHPRCERRNSNVSAQSSRMVPGPLPANGKMHSTVDCNGVYSLGTTT 660
QY 494 -----KRLSQ-NLPVDLDFDEHVDPLHQRALSASVILTTIQOEKQFQPCPCGKNLA 546
D 661 ETEVRKRLSSYQISMEMLE---DSSGRQAMSIASILTNTMEELESROKPCPCWYRFA 717
QY 547 SKYLVWDCSPOMLCIKKVLRTIMTDPFTLAIITICIIINTVFLAVEHNMMDNLTKLI 606
D 718 NVFLWDCDCLVKKVHLNLIIVMDPFVLDLITICIVLTFMAHEHPTMQSSSVLT 777
QY 607 GNWVFTGIFTAEMCKIITADDPYHFRHGNVFDISVALLSLADY-LYNTLSDNNRSLA 665
D 778 GNWVFTGIFTAEMCKIITADDPYHFRHGNVFDISVALLSLADY-LYNTLSDNNRSLA 665
QY 666 SLRVLRFKLAASVPTLNTLKIIGHSVGALGNLTIVLTIVVTFVSVGMRLFGTKPNK- 724
D 835 SPRLRVFKLAKSWPTLNLKIIIGNSVGALGNLTIVLTIVVTFVSVGMRLFGTKPNK- 894
QY 725 TAYATQPRRRHMDNPFYHSLVFLVRLTCGEMENMGMODDGSPLCIIVFLINVI 784
D 895 VCKINVOCKLPRHMDNPFYHSLVFLVRLTCGEMENMGMODDGSPLCIIVFLINVI 784
QY 785 GKLVLNLFIALNLSFNSNEEKDGSLEGETRTKTVQLALDRFRRAFSFMLHALQSFCCK 844
D 954 GNLVNLNLFIALNLSFNSNEEKDGSLEGETRTKTVQLALDRFRRAFSFMLHALQSFCCK 844
QY 845 CRRK---NSPKPKETTESFAGENKDSILPDARPKWEYTDMLYTGQAGAPLAEVIED 901
D 901 CRRK---NSPKPKETTESFAGENKDSILPDARPKWEYTDMLYTGQAGAPLAEVIED 901

Query Match

48.9%; Score 4489.5; DB 2; Length 1983;

Db 1008 CFRKAFFRKPVKVIEIQEG-----NKIDSCMSNNTG-----IEISK 1042
Qy 902 DVEYCGEGALPTSQHSAGVQAGD-----LPPENKQLTSP-----DDQG 940
Db 1043 ELNYLKDNGT-----TSGVGTGSVEKYVIDENDYMSFINPSLTVTVPIAVGESDEN 1097
Qy 941 VEMEVSFSEDLHLSTQSRKSDAVSMLSEGTDLNDFRNLQKTVSPKK--QPDRCFF 998
Db 1098 LNTFEFSSES---ELEESKEKLNATSS--SEGSTDVAPRREGQAEIEPEEDLXPEACT 1153
Qy 999 KGLSCHFLCHTKDRKSPWLWNNTRKTCYOIVKHSWFESFIIFVILLSSGALIFEDVNL 1058
Db 1154 EGCIKKFFPCQVSTBEGKGKIWNLRKTCYSIVHNWPEFETIVFMILLSSGALAFEDIYI 1213
Qy 1059 PSRQVEKLLRCTONIFITFILLEMLKWAFAFGRRYFETSACWLDLFIIVVSVLSLM-- 1116
Db 1214 EORTKTKMVEYADVKTFFIIFILEMLLKWAVGFTYFTNAWCWLDLFIIVDVSVLSVAN 1273
Qy 1117 -----NLPSLKSFRRLRALRALSQFEGMKVYVYALISAIPALNVLVCLIFWLVC 1171
Db 1274 ALGYSELGAIKSLRLRALRALSREFGMRVNVNVALGAIPIIMNVLLVCLIFWLIFS 1333
Qy 1172 ILGVNLFSGKGRGCIINGTDINWLDTEVPNRSCNI---SNYSWKVPQVNDNNGNAYLA 1229
Db 1334 IMGVNLFAKGFYHCVNTTGTGNF-EIKEVNNFSDCQALCKQARKNKNVNDNNGAGYLA 1392
Qy 1230 LLOVATYKGLFIMNAADVSREKDEQDPFEANLYAYLVFVFIIFGSEFTLNLFVGIID 1289
Db 1393 LQOVATFGWMDIMYAAVDSRDVKLOPIYEENLYWLVFVFIIFGSEFTLNLFVGIID 1452
Qy 1290 NFNOQKRLGGDIFMTQEOKKYVYNAKMLGKTKPKQKIPRPLNCKQAFVDFLVTQVFD 1349
Db 1453 NFNOQKKEGGDIFMTQEOKKYVYNAKMLGSKPKQKIPRANKFQGMVDFVTRQVFD 1512
Qy 1350 VIILGLVNLIMMAESADQPKVKTFDILNTAFVVFVIFTECLIKVFALRQHYFTNCW 1409
Db 1513 ISIMILICLNMVTMMVETDDQSKYMTLVLSRLNLFVFLVTFGEFLKLKLSLRYVFTIGW 1572
Qy 1410 NLFQCVVVLSTISLTVLSRL-EDSDISFPPTLFRVVRRLARIGRILLYRAARGITLFA 1468
Db 1573 NIFQFVVVLSVIGVFLAELEKIEFVS--PTLFRVIRLARIGRILRILKAGKINTLFA 1630
Qy 1469 LMMSLPSLNFGLLLFLVWFYIATFGMSWFSKVRKKGSDIDDFNPFETFGSMCLFQITTT 1528
Db 1631 LMMSLPALFNGLLLFLVWFYIATFGMSNFAVYKKEAGIDDFNPFETFGSMCLFQITTT 1690
Qy 1529 SAGWDTLNLPMLEAKE-----HCNSSQSDSCQOPOIAVYFVSYIIISFLIVVNNYI 1580
Db 1691 SAGWDTLNLPMLEAKE-----HCNSSQSDSCQOPOIAVYFVSYIIISFLIVVNNYI 1750
Qy 1581 AVILENFNTATEESDPLGEDDFEIFYEWEKFDPEASQFTQYSALSDFADALPEPLRVA 1640
Db 1751 AVILENFNTATEESAEPSUEDDFEFYEWKFDPDATQFTEFKLSDFAAALDPPPLLIA 1810
Qy 1641 KPNKQFLVMDLPMVNGDRLLHCDMVLFAFTRVLVSSGLDTMTKMTMEKEKFEANPEKKL 1700
Db 1811 KPNKQFLVMDLPMVNGDRLLHCDMVLFAFTRVLVSSGLDTMTKMTMEKEKFEANPEKKL 1870
Qy 1701 YEPVITTTKREEOGAAVIOARVKKHMEKMWKURLKDRSS 1741
Db 1871 YEPVITTTKREEOGAAVIOARVKKHMEKMWKURLKDRSS 1808

RESULT 9

B25019
sodium channel protein II - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C:Accession: B25019; S24804
R:Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.
Nature 320, 188-192, 1986
A:Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A:Reference number: A93377; MUID:86146901

A:Accession: B25019
A:Molecule type: mRNA
A:Residues: 1-2005 <NOD>
A:Experimental source: brain
R:Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
submitted to the EMBL Data Library, August 1991
A:Description: Developmentally regulated RNA splicing of rat brain sodium channel mr
A:Reference number: S24803
A:Accession: S24804
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 183-188, 'D', 190-305 <SAR>
A:Cross-references: EMBL:X61149; NID:g57074; PIDN:CAA43458.1; PID:g57076
C:Superfamily: sodium channel protein
C:Keywords: duplication; ion transport; sodium channel; transmembrane protein; volta

Query Match 48.9% Score 4484.5; DB 2; Length 2005;
Best Local Similarity 48.1%; Pred. No. 0;
Matches 950; Conservative 278; Mismatches 448; Indels 301; Gaps 38;

Qy 11 PDERNRPFTSDSLAAIKKRIAOK-----ERKSKDKAAAEOPRQOLDKASRKLPK 64
Db 9 PGDSFRFRTRESLAAIEQRIAEKAKRPQKERKDEDD-----ENGPKPNSDLEAGKSLPF 64
Qy 65 LYGDIPPELVTKPLEDDPYKDKHKTVMVANKRTIYRFSAKRALFILGPNPLRSLMR 124
Db 65 IYGDIPPELVTKPLEDDPYKDKHKTVMVANKRTIYRFSAKRALFILGPNPLRSLMR 124
Qy 125 ISVHSVSMFTICTVINCMEFMANSMERSFNDPIEYVFIGIYILEAVIKILARGFIVDE 184
Db 125 ILVHSLFNVLMCTILTNCFVMTKSNPPDWTKNV-EYFTGTGIYFESLIKILARGFCLEED 183
Qy 185 FSFLRDPNWLDFVIGTAIATCFPGSOVNLISALRTFRVFRALKAISVISGLKVIVGALL 244
Db 184 FTFLRNPWNWLDFTVITPAYVTEFV-NLGNVSALRTFRVFRALKTISVIGLKTIVGALI 242
Qy 245 RSVKKLVDVWLVTLFCISIFALVGOOLPMGLNCKIKHNCGPNPASN----- 292
Db 243 QSVKKLSDVMLTVCLSVFALIGLQFLNLRNKLQW-----PPDNRSTFINTSFTFN 297
Qy 293 -----KDCFEKEDSEDEIMCGTWLGRPCPNCGSCDKTT 327
Db 298 NSLDNNGTAFNRTVNMFMNWEYIEDKSHFYFLEGONDALLCGNSSDAQCPGYICVKG 357
Qy 328 LNPNNYTKFNFNGSFLAMPFRVMTQDSWERYLROILRTSGIYFVFFVWVIFLGSFYLL 387
Db 358 RNPNYGYTSFTTFSWAFSLFRLMTQDFWENLYQLTLRAAGKTYMIFFLVIFLGSFYLI 417
Qy 388 NLTLAVVTMAYEEQNRNVAAETAEKEMFOE-AQOLLREEKEALVAM----- 433
Db 418 NLILAVMAYEEQNRNVAAETAEKEMFOE-AQOLLREEKEALVAM----- 477
Qy 434 -GIDRSSLNSLQASSFSFKPKKFFGSKTRK----- 462
Db 478 GGIGVFSESSVASKLSSEKELKNRKKKKQKEOEKEEDAVRKSASEDSIRKKGF 537
Qy 463 SFFWRGSKTAQ----- 482
Db 538 QFLEGSRLTYEKRFSPSPHQSLLSTIRGSLFSPRRNSRSLFNFKGRVKDIGSENDADDE 597
Qy 483 -----ASKNPQLLEOTKRLSONLPV----- 502
Db 598 HSTFEDNDRSDSLFVPHRHGERRPSNVSQASRASRGITPLPMNCKMHSAVDCNCGVSVSLV 657
Qy 503 -----DLFDE-----HV-----DPLHRQRALSVAISILTIQ 529
Db 658 GGPSALTSVQQLLEPGTTTETETIKRKRSSSYHVSMDLEDP-SQRAMSMASILNTME 716
Qy 530 EOEKQFQPCFCGKNLASKYLVWDCSPOWLCKIKVLRITMTDPTTELATITCIINTVFL 589
Db 717 ELESROKCPCKWKFKANMCLIMWDCCKPWLKVHVNVLVMDPFDVLAITITCIIVLNTLFM 776

Qy 590 AVEHNNDNKTILKIGNWVGTGIFIAEMCLKIITDLPYHYFRHGNVWFDSIVALLSLA 649
Db 777 AHEHYPTMEQFSSVGNLVGTGTAEMFLKIIITAMPDYFYFQEGWNIIDGFIYLSLM 836
Qy 650 DV-LYNTLSNDRSLASIRLVLPFKLAKSWPTLNTLKIISHSVGALGNLTIVLTV 708
Db 837 ELGLANV---EGLSVLRFRLLRVFKLAKSWPTLNLKIIIGNSVGLGNLTIVLTV 893
Qy 709 IFSVGMRLFGTKFNKTAYATQ---ERPRRRWHMDNPFYHSFLVPRILCGEWIENWGM 765
Db 894 IFAYVGMQLFGSKYECVCKISNDELP--RWHMHDFEHSFLVPRILCGEWIENWGM 951
Qy 766 QDMGSPICIIIVFIMVIGKLVNLFIALNLSFNEEDKGSLEGTRTKTKVOLALDR 825
Db 952 -EVAGTMCITVFMVMVIGLVNLFIALNLSFSSDNL-AAADDNDDNNMLQIAVGR 1009
Qy 826 FRRASFEMHALQSPCKCKRKNP---KPKETTESFAGENKDSILDPARPKKEYD 881
Db 1010 MOKGIDFVKRIRFQAFVKQKALDEIKPLEDNN---KKDSCISN----- 1055
Qy 882 MALVTGAGAPLAPLAIVEDDVEYCGEG---GALPTSOHSAGVQAGD---LPPETKQL 933
Db 1056 -----HTTIEIGKDLNLYKDCNGITSGIGSSVEKYVYVDESVMFINNPSLTV 1103
Qy 934 TSP-----DOGVEMEVSEEDLHLSIQSPRKSDAVMSLSECTIDLNDIFRLQKTV 987
Db 1104 TVPIALGESDFENLTESFSES---DMEESKEKLNATSS-SEGSTVDIGAPAEQPEA 1159
Qy 988 SPKK--OPDRCPKGLSCHFKCHTKDRKSPVLMWNRKTCYQIVKHSWESFIIFVIL 1045
Db 1160 EPESELEPEACTEDCVKRFKCCQISIEEGKGLMNRKTCYKIVENHWFETTFVFMIL 1219
Qy 1046 LSSGALIFVNLPRPOVEKLRCTDNIFIFILEMLKWAFFRFRYTSAMCWLDF 1105
Db 1220 LSSGALAFEDIVIEQRTIKTLEADKVYFIIFILEMLKWAFFRFRYTSAMCWLDF 1279
Qy 1106 LIVVSVLSL-----NMLPSLKSFRTLRALRPLRALSQFGMKVYVALISATPILN 1158
Db 1280 LIVDVSLSLTANALGYELGAIRKLRTRALRPLRALSFRFGMKVYVALISATPILN 1339
Qy 1159 VLLVCLIFWLVFCLGVNLFSGKFCRCINGTDINMLDFTVPRNSQCN---SNYS--W 1213
Db 1340 VLLVCLIFWLVFCLGVNLFSGKFCRCINGTDINMLDFTVPRNSQCN---SNYS--W 1213
Qy 1214 KPVQNFNDVNGYALLOVATYKGLWLEIMAAVDSREKDEQPEANLYAYLYEWFVFI 1273
Db 1399 KNVKYNEDNVLGYSLLLOVATYKGLWLEIMAAVDSREKDEQPEANLYAYLYEWFVFI 1458
Qy 1274 FGSFTLNLFGVITIDNNOQKKLGQDIFWTEBQKYYNAMKLGKTKPKQPIPRPLN 1333
Db 1459 FGSFTLNLFGVITIDNNOQKKLGQDIFWTEBQKYYNAMKLGKTKPKQPIPRPLN 1518
Qy 1334 KQAFVFDLVTQVDFVILGLVNLMIIMAESADQPKVKKTFDILNIAFVFIETEC 1393
Db 1519 KQGVVFDVTKQVDFVILGLVNLMIIMAESADQPKVKKTFDILNIAFVFIETEC 1578
Qy 1394 LKVPALRQHYFTNGWNLFDVNVLSIITSLVSLR-BDSISPPPTLFRVVRRLARIGRI 1452
Db 1579 VLKLSLRHYFTNGWNLFDVNVLSIITSLVSLR-BDSISPPPTLFRVVRRLARIGRI 1636
Qy 1453 LRLVRAARGIRTLFPALMWSPLFNIGLILFLVNFYIAFGMSWFSKVKSGGIDIDFN 1512
Db 1637 LRLKAGKIRTLFPALMWSPLFNIGLILFLVNFYIAFGMSWFSKVKSGGIDIDFN 1696
Qy 1513 PETFTGSMCLFQITTSAGWDTLLNPMLEA-----KEHNSSSQSCQOQPIAVYVF 1564
Db 1697 PETFTGSMCLFQITTSAGWDTLLNPMLEA-----KEHNSSSQSCQOQPIAVYVF 1756
Qy 1565 VSYIIISFLVNMVYIAVILENFNTATESEDPLEGGDFEIFYEYWEKFDPEASQFIQYS 1624
Db 1757 VSYIIISFLVNMVYIAVILENFNTATESEDPLEGGDFEIFYEYWEKFDPEASQFIQYS 1816
Qy 1625 ALSDFADALPEPLRVAKPNKQFLVMDPLPMVNGDRLHGMVLFATFTTRVLGSDSLDTMK 1684

Db 1817 KLSDEFAAALDPPLLIATAKPNKQFLVMDPLPMVNGDRLHGMVLFATFTTRVLGSDSLDTMK 1876
Qy 1685 TMMEKEKFEANPPFKLYEPIVTTTTRKKEEEOGAAVIOARAYRKHKMEKMLKRLKDRSS 1741
Db 1877 IQMEERFASNPSPKSVSEPIPTTTLARKQOEVAIVIOARIRY---LLKQKVKVYSS 1930
RESULT 10
A:25019
A: sodium channel protein I - rat
A: Alternate names: sodium channel protein A
A: Species: Rattus norvegicus (Norway rat)
A: Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
A: C: Accession: A25019; S40783; I84764
A: Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.
A: Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A: Reference number: A93377; MUID:86146901
A: Accession: A25019
A: Molecule type: mRNA
A: Residues: 1-2009 <NOD>
A: Cross-references: GB:X03638; NID:g57216; PIDN:CAA27286.1; PID:g57217
A: Experimental source: brain
A: Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
A: Nucleic Acids Res. 19, 5673-5679, 1991
A: Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel.
A: Reference number: S40782; MUID:92051314
A: Accession: S40783
A: Molecule type: DNA
A: Residues: 177-253 <SAR>
A: Noda, M.; Numa, S.
A: Title: Recept. Res. 7, 467-497, 1987
A: Title: Structure and function of sodium channel.
A: Reference number: I50536; MUID:87311395
A: Accession: I84764
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-2009 <RES>
A: Cross-references: GB:M22253; NID:g1041088; PIDN:AAA79965.1; PID:g1041089
A: Superfamily: sodium channel protein
A: Keywords: duplication; ion transport; sodium channel; transmembrane protein; volta

Query Match 48.8%; Score 4476; DB 2; Length 2009;
Best Local Similarity 47.9%; Pred. No. 0;
Matches 942; Conservative 289; Mismatches 444; Indels 292; Gaps 39;

Qy 11 PDERNFRPTSDSLAAIKKRIAIQERKKSKDKA-AAEPQPRPQLDLSKSRKLPKLYGDI 69
Db 11 PDSFNF--FTRESLAAIERIAEAEKAKNPKDPKDDDENGPKPNSDLEAGKNLPFIYGI 68
Qy 70 PPELVTKPLEDLDPYKDKHTFMVNLKRTYRFSAKRALFILGPNPLRLSMLIRISVHS 129
Db 69 PPEMVSEPLEDLDPYKDKHTFMVNLKRTYRFSAKRALFILGPNPLRLSMLIRISVHS 128
Qy 130 VFSMFLICITVIINCVMANSMERSFDNDIPEVVFVIGVILEAVIKILARGFTVDSFSLR 189
Db 129 LFSMLIMCTILTNVCFMTMSNPDPWTKNV-EYFTFTGFTFESLIKIIARGFCELDFTFLR 187
Qy 190 DPWNMLDFTVIGTATATCFPGSQVNSALRTPFRFRALKAIISVIGLVKIVGALLRSVKK 249
Db 188 DPWNMLDFTVITFAVYTEV-DLGNVSALRTPFRFRALKAIISVIGLVKIVGALLRSVKK 246
Qy 250 LVDMVNLTLFCLISIFALVQQLFMGLINQKCI-----KHNGPNPAS-----N 292
Db 247 LSDVMILVCLVSEFALIGLQFLMGLNRKNCVQWPTNASLEHSTEKNTVDYNGTLVN 306
Qy 293 KDCFEKE-----KDE-----DFMCGTWLSRCPNCGSTCDKTTLNPNNTKPD 338
Db 307 ETVFEDFKSKYIQDSRYHYFLEGLDALLCGNSSDAGOCPEGYCMCKAGRNNGYTSFD 366
Qy 339 NFGWSFLAMFRVMTQDSMERLYRQILRTSGIYFVFVFFVIFLGSFYLLNLTLAVVTMAY 398

Db 367 TFSWFLSLFRLMTODFENLYQLTLRAAGKTYMIFFLVFLGSLYLINLILAVAMAY 426
QY 399 EEOHNRVAATEAKEMQEQAOQLLREEKEAL-----VANGIDRSSLNS 442
Db 427 EEOHNRVAATEAKEMQEQAOQLLREEKEAL-----VANGIDRSSLNS 486
QY 443 LQASSFSFKRK-----FGSKT-----RKSEFM----- 466
Db 487 SKLSSKAKERRNRKRRKQKQEQSGEKKDDDFHFKSESDSIRKGRFSGIEGNRLTYE 546
QY 467 -----RGSKT-----AQASASDSEDDASKNP 487
Db 547 KRYSSPHQSLLSIRGSLSPRRNSRSLSPFRGRAKDVSENFADDEHSTFEDNESRRD 606
QY 488 QL-----LEOTKRLS-----Q 498
Db 607 SLFVPRRHRGRRNSLSQTSRSSRLAGLPANGKMHSTVDCNGVSVVGGSPVTPSPVQ 666
QY 499 NLPVDLDFE-----HV-----DPLHROALSAVSILITITIOE 530
Db 667 LLPEVIIDKPADTNGTTTETEMKRRSSSFHVSMDFLEDFSQRORAMSIASILNTVEE 726
QY 531 QEKQEPCCPKCNILASLYWDCSPQWLCIKKVLRTIMTDFTELAITICIIINTVFLA 590
Db 727 LEESRQKPCPCWKYFSNIFLWDSPYWLKVKHIVLVVMDPFVLAITICIVLTLFMA 786
QY 591 VEHNMDNLLKILKIGNVWTGFIABMKLITLADPDPHYFRHGWVDFSDVALLSLAD 650
Db 787 MEHYPTMEHNVLTGVLVGTGFIABMKLITLADPDPHYFRHGWVDFSDVALLSLAD 846
QY 651 V-LYNTLSDNNRSLASLVRVFKLAKSWPTLNTLKIIGHSVGALGNLWTLTVVFI 709
Db 847 LGLANV-----EGLSVLSRFLRLRVFKLAKSWPTLNTLKIIGHSVGALGNLWTLTVVFI 903
QY 710 FSVGMRLFGTKFNKTA--YATQ--ERPRRRWHMDNFYHFLVFRILCGEWNENMGCMQ 766
Db 904 FAVVGMQLFGSKYKDCVKIATDCKLP--RWEMDNDFHSLFIVRVLGCEWETWDMCM- 960
QY 767 DWDGSPCLIVFLVWIKLVNLFTALLNFSNEEKDGSLEGETRKTKVOLALDRF 826
Db 961 EVAGQAMCLTVFMVMVVRNLVNLFLALLLSFSADNL--AATDDDDNEMNLQIAVDRM 1019
QY 827 RRAFSEMLHALQSFCKCKRKNPKPKETTESFAGENKDSILDPARWKEY----DTDM 882
Db 1020 HKGVAYYKRIYEF-----IQSFV--RKQILDEIKLDDLNLNRKDNCT 1062
QY 883 ALYTGQAGAPLAPLAEDVVEYCEGGL-----PTSQHSAGVQAGDL 926
Db 1063 SNHTTEIGKDLCKLDVNGTSGIGTSSVEKYIIDESDYMSFINNPSTVTVPIAVGE- 1121
QY 927 PPEIKQLTSPDQGVEMEVSEEDLHLSIQSPRKSDAVSMLSECTSIDLNDIFRNLOKT 986
Db 1122 -----SOFENLNTDFSES-----DLESSEKLNSSSSSGSTVDIGAPAE-OPV 1168
QY 987 VSPKK--OPDRCPFKGLSFCHKTDRKSPWVLMWNRITCQIVKHWSFESFIIFVI 1044
Db 1169 MEPETLEPEACFTGCVQRFKCCQISVEEGRGKQWNLRTCTFRIVEHNFETFIIVMI 1228
QY 1045 LLSGALIFEDVNLPSRQVEKLLRCDTNIETFIPLLEMLKWWAFGRFRRTYSACWCLD 1104
Db 1229 LLSGALAFEDIYDQRTIKTLMLEYADKVFTYIFILEMLLKWVAYGYQTYFTNACWCLD 1288
QY 1105 FLIVVWSVLSL-----MNLPSLKSFTLRALPLRALSQFEGMKVVVYALISAIPAIL 1157
Db 1289 FLIVDVSLSVTANALYSSELGALKSLRTRALRPLRALSFEGRVVRVNNALLGAIPSIM 1348
QY 1158 NVLLVCLIFLWVFCILGNLFSGRFGRCINGTDINMYLDTFVFNRSQC-----NISNYS 1212
Db 1349 NVLLVCLIFLWVFCILGNLFSGRFGRCINGTDINMYLDTFVFNRSQC-----NISNYS 1407
QY 1213 WKVQVQVNDVGNVYALLQVATYTKGWLIEIMNAAVDSRDEQDQDFEANLYAYLYFVVFI 1272
Db 1272 WKVQVQVNDVGNVYALLQVATYTKGWLIEIMNAAVDSRDEQDQDFEANLYAYLYFVVFI 1272

Db 1408 WKNVKNVNDNVGFGYLSLQVATEKGMWDMIMYAAVDSNRVELQPKYEEESLYMYLVFVFI 1467
QY 1273 IFGSFPTLNLFGIYIIDNFNOOKKLGQDIFMTPEQKYYNAMKKLTKPKQKPIPRPL 1332
Db 1468 IFGSFPTLNLFGIYIIDNFNOOKKLGQDIFMTPEQKYYNAMKKLTKPKQKPIPRPG 1527
QY 1333 NKCOAFVFDLVTQVDFVILILVNLMIIMMAESADQPKDKVTFDILNIAFVVFITJE 1392
Db 1528 NKFGQVDFVTRQVDFISIMILICLNMVYMWVETDDQSDYVTSLSRLNLFVIFVITGE 1587
QY 1393 CLIKVAFALRQHYFTNGWNLFDVCVVVLSIISTLVSL--EDSDISFPPTLFRVRLARIGR 1451
Db 1588 CVLKLSLRHYFTNGWNLFDVCVVVLSIISTLVSL--EDSDISFPPTLFRVRLARIGR 1645
QY 1452 ILRLVRAARGIRTLFALMMSLPSLFNIGLGLLFVWFIYAFPGMSWFSKVKKSGSIDDI 1511
Db 1646 ILRLKAGKIRTLFALMMSLPSLFNIGLGLLFVWFIYAFPGMSWFSKVKKSGSIDDI 1705
QY 1512 NFETFTGSMCLFQITTSAGWDTLLNPMLEAK--EHCN-----SSSDSCQOPOIAVY 1563
Db 1706 NFETFTGSMCLFQITTSAGWDTLLNPMLEAK--EHCN-----SSSDSCQOPOIAVY 1765
QY 1564 FVSYIIISFLVNMVYIAVILENNTATESEDEPLGEDDFEIFYEVWEKFDPEASQFIQY 1623
Db 1766 FVSYIIISFLVNMVYIAVILENNTATESEDEPLGEDDFEIFYEVWEKFDPEASQFIQY 1825
QY 1624 SALSDFADALPEPLRVAKPNKFQFLVMDLPVWMDRLHMDVLPFAFTTRVVLGDSGLDTM 1683
Db 1826 EKLQSOFAALPEPLRVAKPNKFQFLVMDLPVWMDRLHMDVLPFAFTTRVVLGDSGLDTM 1885
QY 1684 KTMKEKMEANPKPKLYPIVTTTKRKEEQGAIVQIARVYKHKMEK 1730
Db 1886 RQMEERFMAENPKPKLYPIVTTTKRKEEQGAIVQIARVYKHKMEK 1932
RESULT 11
CHRTM1
sodium channel protein mul alpha chain, skeletal muscle - rat
C:Species: Rattus norvegicus (Norway rat)
Q:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 22-Jun-1999
C:Accession: JN0007
R:Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.;
Neuron 3, 33-49, 1989
A:Title: Primary structure and functional expression of a mammalian skeletal muscle
A:Reference number: JN0007; MUID:90148778
A:Accession: JN0007
A:Molecule type: mRNA
A:Residues: 1-1840 <TRI>
A:Cross-references: DB:M26643; NID:g205651; PIDN:AAA41682.1; PID:g205652
C:Comment: Action potentials propagated by skeletal muscle sodium channels are respon-
C:Comment: This heavily glycosylated protein contains four homologous domains, each
C:Comment: This protein is distinct from but related to sodium channel proteins isol-
C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phospho-
F:120-458,561-813,1013-1305,1335-1611/Region: duplication
F:56,251,1321,1504/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase)
F:214,288,291,297,303,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site:
Query Match 47.6%; Score 4363.5; DB 1; Length 1840;
Best Local Similarity 49.3%; Pred. No. 2.8e-316;
Matches 908; Conservative 275; Mismatches 427; Indels 233; Gaps 35;
QY 11 PDENFRFTSDSLAAIKKRIATQKCK--KSKDKAAAEQPRPOLDLKAASKRLPKLYGD 68
Db 12 PGPHCLRFTESLAAIEQR-AVEEARLQNKQMEIEPERKPRSDLEAGKNLPIYGD 70
QY 69 IPPELVTKPLDLPYKDKHTFMVNLKRTIYRFSAKRALFILGPNPLSLMIRISVH 128
Db 71 PPPEVIGLPELDPYKDKHTFMVNLKRTIYRFSAKRALFILGPNPLSLMIRISVH 130
QY 129 SVFMSFICTVIINCMMFMANSMERSFNDIPEYVFIGIYILEAVIKILARGFVDFEFL 188
Db 188 SVFMSFICTVIINCMMFMANSMERSFNDIPEYVFIGIYILEAVIKILARGFVDFEFL 188

Db 131 ALPSNFMITILLNCVPMWMSNPPSWSKHV-EYTFGTGIYTPESLIKMLARQFCIDDTFEL 189
Qy 189 RDPNWLDFIVIGTAIATCFPGSOVNLISALRTERFRVRAKKAISVISGKIVTGALLRSVK 248
Db 190 RDPNWLDFIVIGTAIATCFPGSOVNLISALRTERFRVRAKKAISVISGKIVTGALLRSVK 248
Qy 249 KLVDVWVLTFLCLSFALVGOOLPMGLNOKICKHNGCPNPASN----- 292
Db 249 KLSVDMILTFLCLSFALVGOOLPMGLNOKICKHNGCPNPASN----- 305
Qy 293 -----KDCFEKE-----KDSDEFMCGPWLGRPCPN 319
Db 306 WYGNWTWYINDTWNSQESWAGNSTFDWEAYINDEGNFYFLEGSNDALLCGNSSDAGHCP 365
Qy 320 GSTCDKTLTLPNDNNYTKDFNGSWFLAMFRVMTQDSWERYLRQILRTSGIYFVFVVVI 379
Db 366 GYECIKAGRPNYGYTSDYDFSWAFALFLRLMTQDYENLFLQTLRAAGTKYMIFFVVII 425
Qy 380 FLGSFYLLNLTLAVVTWAYEQNRVAAETAEKMFQEAQOQLLREBEKALVANGIDRSS 439
Db 426 FLGSFYLLNLTLAVVTWAYEQNRVAAETAEKMFQEAQOQLLREBEKALVANGIDRSS 476
Qy 440 LNSLQASSFSFKRRKFGSKTRKSFMRGSKTAOASASDSDASKNPQLLEQTKRLSQN 499
Db 477 -----EKAQAALSGEADG-----DPTHNKDCN 502
Qy 500 LPVDFDEHVDLHRQRALSAVISLITITIQOERKFPQPCPGKNLASKYLVWDCSPOWL 559
Db 503 GSLDASGEKGP---RFSQSADSALSADAMELEAHQKCPWYKCAHKVLIWNCAPW 559
Qy 560 CIKVLRTMTDPTTELAITICIIINVTFLAVEHHNDMDNLTILKTNWVFTGIFTAEM 619
Db 560 KFKHIIIVLMDPVDLGITITICIIINVTFLAVEHHNDMDNLTILKTNWVFTGIFTAEM 619
Qy 620 CLKTIADDPHYFRHGNVDFSIALLSLADV-LYNTLSDNNRSLASRLVRFKLA 678
Db 620 VLKLIADDPHYFRHGNVDFSIALLSLADV-LYNTLSDNNRSLASRLVRFKLA 676
Qy 679 WPTLNTIKIIGHSGVAGLNLTVLTIVFISFVVGMLRFTGKFNK-TAYATQBRPRRW 737
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Qy 738 HMDNFYSFLVFRILCGEWITENMWMQMDGMDGSPCLTIIVFLVIMVIGKVLVNLFTALL 797
Db 737 HMDNFYSFLVFRILCGEWITENMWMQMDGMDGSPCLTIIVFLVIMVIGKVLVNLFTALL 795
Qy 798 LNSFSNE-----EKDGSLEGETRKYQLALDRER---RAFSPMLHALQSFCKCKCRK 848
Db 796 LNSFSNE-----EKDGSLEGETRKYQLALDRER---RAFSPMLHALQSFCKCKCRK 840
Qy 849 NSPKPKETTESF-----AGENKDSILPDARPKWKEYDTDMAL-----YTGQAGAPLA-- 894
Db 841 KILSPKEIILSLGEPGAGANAESTPEDEKKEPPEDKELKDNHILNHVGLTDPGRSSI 900
Qy 895 -----PLAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPETKOLTSPD 937
Db 901 ELDLNFINNPLYTIQVPIASESDLE-----MPTEE----- 932
Qy 938 DOGVEMEVFSE-EDLHLSIQSPRKSDAVSMLSECSTIDLIDIFRNLOKTV--SPK-KQP 993
Db 933 -----ETDAFSEPDIKPLQPLQDGNSSV-----CSTADYKPPEDPEEQAEENPEGQP 983
Qy 994 DRCPKGLSCHFLCHKTKDRKSPWLVWNNIRKTCYQIVKHSWFESFIFVILLSGALIF 1053
Db 984 EECFEACVRCPCLYVDISGRCKMWTLRACEKIVEHWFETTFVIMLILLSGALAF 1043
Qy 1054 EDVNLPSRPOVEKLLRCDNTIFTFLEMLKWWAFGRFRYFTSAMCWLDFLIVVSVL 1113
Db 1044 EDVIEQRRVIRTILEYADKVTFVIFILEMLKWWAFGRFRYFTSAMCWLDFLIVVSVL 1103
Qy 1114 SLM-----NLPSLKSFTRLRALRPLRALSOFEGMKVYVALISAPAILNVLVCLIF 1166
Db 1104 SLVANWLGYSPLGPKILRLRALRPLRALSOFEGMKVYVALISAPAILNVLVCLIF 1163

Qy 1167 WLVEICILGVNLFSGKFGRCINGTODINMYLDFTEVPNRSQCNISNYS-----WKVPQVNFN 1222
Db 1164 WLVEICILGVNLFSGKFGRCINGTODINMYLDFTEVPNRSQCNISNYS-----WKVPQVNFN 1222
Qy 1223 VGNAYLALLOVATYKGLWLEIMNAADVSRKDEQDFEALYALYFVFIIFGSEFTLNL 1282
Db 1223 VGNAYLALLOVATYKGLWLEIMNAADVSRKDEQDFEALYALYFVFIIFGSEFTLNL 1282
Qy 1283 FIGVIDNFNOOKKLGODIFMTTEOKKYNNAMKLGCTKPKQPIRPLNKNCOAFVDEL 1342
Db 1283 FIGVIDNFNOOKKLGODIFMTTEOKKYNNAMKLGCTKPKQPIRPLNKNCOAFVDEL 1342
Qy 1343 VTSQVEDVILIGLIVLNMIMMAASADQPKDKTKFDL---NTAFVVIIFTIECLIKVFA 1399
Db 1343 VTSQVEDVILIGLIVLNMIMMAASADQPKDKTKFDL---NTAFVVIIFTIECLIKVFA 1399
Qy 1400 LRQHYFTNGWNLFDVGVVLSIITSLVSRLEDSOISFPPTLFRVRLRARIGRILRLVRAA 1459
Db 1400 LRQHYFTNGWNLFDVGVVLSIITSLVSRLEDSOISFPPTLFRVRLRARIGRILRLVRAA 1458
Qy 1460 RGIRTLFALMMSLPSEFNIGLILFLVMFIYAFMGSMFVKVKGSGIDIDFNPFETFGS 1519
Db 1459 RGIRTLFALMMSLPSEFNIGLILFLVMFIYAFMGSMFVKVKGSGIDIDFNPFETFGS 1518
Qy 1520 MLCLFOITTSAGWDTLNLMLEA-----KEHCNSSQSDSCQOQIAVVFVSYIIS 1571
Db 1519 MLCLFOITTSAGWDTLNLMLEA-----KEHCNSSQSDSCQOQIAVVFVSYIIS 1578
Qy 1572 FLIVVNYIAVLENFNTATESEDEPLGEDDFEIPFYEWKEDFPASOFIQYSALSADPAD 1631
Db 1572 FLIVVNYIAVLENFNTATESEDEPLGEDDFEIPFYEWKEDFPASOFIQYSALSADPAD 1638
Qy 1632 ALPPLRVRKPKFQFLVMDLPMVMDRGLHMDVLFATFTRVLGSSGLDGMTWEEKF 1691
Db 1632 ALPPLRVRKPKFQFLVMDLPMVMDRGLHMDVLFATFTRVLGSSGLDGMTWEEKF 1698
Qy 1692 MEANPFKLYEPIVTTTKRKEEEOGAAVIOYAIRYKH-MEKVVK 1733
Db 1692 MEANPFKLYEPIVTTTKRKEEEOGAAVIOYAIRYKH-MEKVVK 1733
Qy 1699 MAANPSKVSYPEITTLTKRKEEEOGAAVIOYAIRYKH-MEKVVK 1741
Db 1699 MAANPSKVSYPEITTLTKRKEEEOGAAVIOYAIRYKH-MEKVVK 1741

RESULT 12

164893

sodium channel alpha subunit - human

C:Species: Homo sapiens (man)

C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 20-Aug-1999

C:Accession: 164893

R:George, A.L.

Ann. Neurol. 31, 131-137, 1992

A:Title: Primary structure of the adult human skeletal muscle voltage-dependent sodi

A:Reference number: 151964; MUID:92246457

A:Accession: 164893

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1836 <RES>

A:Cross-references: GB:M81758; NID:g338212; PIDN:AAA60554.1; PID:g338213

C:Genetics:

A:Gene: Skm1

C:Superfamily: sodium channel protein

C:Keywords: duplication

Query Match 47.5%; Score 4355.5; DB 2; Length 1836;

Best Local Similarity 49.3%; Pred. No. 1.1e-315;

Matches 908; Conservative 271; Mismatches 415; Indels 249; Gaps 35;

Qy 17 RPTFSDSLAAIKKRIAIQKERR--KSKDKAAAEOPRQOLDLKASRKLKLYGDIPELIV 74

Db 18 RPTFSDSLAAIKKRIAIQKERR--KSKDKAAAEOPRQOLDLKASRKLKLYGDIPELIV 76

Qy 75 TKPLEDDPYKYDHTFVNLNKRRTIYRFSAKRALFILGPNPLRSLMIRISVHVSFMF 134

Db 75 TKPLEDDPYKYDHTFVNLNKRRTIYRFSAKRALFILGPNPLRSLMIRISVHVSFMF 134

Db 77 GIPLEDLPYYNKKTFITVLNKGRAIPRESATPALYLSPSVVRRGAIKVLIIHALPSMF 136
QY 135 IICIVINCMPANMERSFNDIPDYVFIGIYILEAVIKILANGFIVDESFLRDPNWX 194
Db 137 IMITILNCVFMTSDPPWSKNV-EXTFTGYTFESLIKILARCFVDDFTFLRDPNWX 195
QY 195 LDFVIGTAIATCPGSONLSALRTRPVFRALKAISVIGSLKVLIVGALLRSVKKLVDVM 254
Db 196 LDFSVMWAYUTEFV-DLGNISALRTRFVLRALKTIIVIPGLKTIIVGALIOSVAKLSLSDVM 254
QY 255 VLTFLCISIFALVQOQLFMGLINOKICKHNCPPNPSN- 292
Db 255 ILTVFCLSVFALVGLQFMGLRQKVR--WPPFENDTNTWYSNDTWYGNEM 311
QY 293 -----KDFEKB----- 311
Db 312 WYGNDSWYANDTWNASHAWATNDFDWDAYTSDGNFYFLEGSNDALLCGNSDAGHCPK 371
QY 320 GSTCDKTTLPNDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIVFVFFVVV1 379
Db 372 GYECIKTCGRNPNYGYSTDSWAFALFRLMTQDYWHENLEQLTLRAAGKTYMIFVVV11 431
QY 380 FLGSYLLNLTLAVVTWAYEONRNVAATEAKEMFOEAQOLLREEKEALVAMGIDRSS 439
Db 432 FLGSYLLNLTLAVVAMAYABQNEATLAEDKEKEEFOQMLEKTKKHOEL----- 482
QY 440 LNSLOASFSFKRKFSGSKTRKSFMRGSKTAQA---SASDEDDASKNPOLLEQTKRL 496
Db 483 -----EKAQAQALEGGEADGDPFAGHKONGCSLDTSQ 515
QY 497 SONLPVDLDFHRQALSAVSILITITIOEQKFQPCFCGKNLASKYLWDCSP 556
Db 516 EKGA-----RQSGSDSGISDAMEELEEAHQKCPWPKYKCAKVLWDCCA 562
QY 557 QWLCKIKVLRITMDPTTELAIITCIIINTVFLAVEHHNMDNLKTLKIGNWFTGIFI 616
Db 563 PWLFKNIILHLVMDPPFDLITICIVLTLFMAMEHYPMTEHFDNVLTVGNLVTGIFT 622
QY 617 AEMCLKIADLPYHFRHGNVFDISVALLSLADY-LYNTLSNNRSLASLRLVLPFKL 675
Db 623 AEMVCLKIADLPYHFRHGNVFDISVALLSLADY-LYNTLSNNRSLASLRLVLPFKL 679
QY 676 AKSWPTLNLTKIIGHSGALGNLTIVLTIVVFISVVGMLFGTKFNK-TAYATQERPR 734
Db 680 AKSWPTLNLTKIIGHSGALGNLTIVLTIVVFISVVGMLFGTKFNK-TAYATQERPR 739
QY 735 RRWMDNPFSLVFRILCGEWIENMMGQMDGSPCLTIIVFVLIMVIGKVLVNLFI 794
Db 740 PRWMDNPFSLVFRILCGEWIENMMGQMDGSPCLTIIVFVLIMVIGKVLVNLFI 798
QY 795 ALLNLSFNE-----EKDGSLEGETRTKVKQALDRFRAPFSF-----MLHALQSFCC 842
Db 799 ALLNLSFNE-----EKDGSLEGETRTKVKQALDRFRAPFSF-----MLHALQSFCC 846
QY 843 KRCRRKNSPKPKETESF-----AGENKDSILDPAR--PWKE---YDTRDMALYTGQA 889
Db 847 -----KILSPKDIWLSGEADGAGEAGETAPDEKKEPPEDLKKNHILNHMGLA 900
QY 890 GAP-----LAPLAEVDDVEYCGGALPTSQHSAGVQAGDLPPEP 930
Db 901 DGPPSSLEHLNFINNPYLTIQVPIASESDLE-----MPTEE-----ET 941
QY 931 KQLTSPDQGVMEVFSEEDHLISQSPRKSDAVMSLSESTIDLNDIFRNLOKTV--S 988
Db 942 DTFSEPED-----SKPPQPLYDGN--SVGSTADYKPPEDPEEQAEEN 984
QY 989 PK-KQPORCFPKGLSCHFLCHTKTKRSPWLVNWNIRKTCVQIVKHWSFESFIIFVILLS 1047
Db 985 PEGQPECECTEACVQRPCLYVDISQGRKKKWTLLRACFKIIVHNWFFFIIVFMILLS 1044
QY 1048 SGALIFEDVNLPSRQVEKLLRCTDNIFTFIFLEMLKWKVAFGRFRYFTSAWCWLDPLI 1107
Db 1045 SGALAFEDIYTEORVIRTILEYAKVFTYIFIMEMLLKWVAYGKVFYFTNACWLDPLI 1104

QY 1108 VVSVLSLML-----NLPSLKSFTLRALRPLRALSQFEGMKVYVYVALISAIPLNLVL 1160
Db 1105 VDSIISLVANWLGVSSELGPIKSLRTRALRPLRALSQFEGMRVYVVALISAIPLNLVL 1164
QY 1161 LVCLIFLWLVFCLIGLVNLFSGKFGRCINGTDINMYLDETFEVPNRSOC-----NISNYSWKVP 1216
Db 1165 LVCLIFLWLVFCLIGLVNLFSGKFGRCINGTDINMYLDETFEVPNRSOC-----NISNYSWKVP 1216
QY 1217 QVNDVNGVAYLALQVATYKGLWEIMNAVDSREKDPQDFEALYLYLVFVFWFIIFGS 1276
Db 1224 KVNVDNVLGLYLSLQVATYKGLWEIMNAVDSREKDPQDFEALYLYLVFVFWFIIFGS 1283
QY 1277 FFTNLFLVIGVVIDNPNQOQKLLGGODIFMTWEEKYKYYNAMKLGTKKQKPTIPRLNKQ 1336
Db 1284 FFTNLFLVIGVVIDNPNQOQKLLGGODIFMTWEEKYKYYNAMKLGTKKQKPTIPRLNKQ 1343
QY 1337 AFVDELTVSQVDFVITLILGLVILNMIIMAESADQPKVKTFDIL--NIAPVVIITTEC 1393
Db 1344 GMVYDLVTQAFDITIMILICLNWTVMTVDDQS--OLKVDILYNINMFIIFTGEC 1400
QY 1394 LIKVFALRQHYFTNGWNLFDVCVVVLSIISTLSVLSLEDSDISFPPTLFRVVLARIGRL 1453
Db 1401 VLKMLALROYFTVGNWIFDFVWVILSVGLALSOLQK-YFVSPTLFRVIRLARIGRL 1459
QY 1454 RLVARARGIRTLFALMMSLPSLNFNIGLILFLVMFIYAFGMSWFSKVKKSGIDDIENF 1513
Db 1460 RLIRGAKGIRTLFALMMSLPSLNFNIGLILFLVMFIYAFGMSWFSKVKKSGIDDIENF 1519
QY 1514 EFTFGSMCLFQITTSAGWDTLNPNLEA-----KEHCNSSQDSQQOQIAVAVFV 1565
Db 1520 EFTFGSMCLFQITTSAGWDTLNPNLEA-----KEHCNSSQDSQQOQIAVAVFV 1565
QY 1566 SYIISFLIVNMYIAVILENPNATATESDPLGDEDDFEIFVYWEKEDPEASQFIQYSA 1625
Db 1580 SYIISFLIVNMYIAVILENPNATATESDPLGDEDDFEIFVYWEKEDPEASQFIQYSA 1639
QY 1626 LSDFADALPEPLRVAKPNKQFLVMDLPMVMGDRHLCHMDVLPFAFTTRVLGSSGLDWTMT 1685
Db 1640 LSDFADALPEPLRVAKPNKQFLVMDLPMVMGDRHLCHMDVLPFAFTTRVLGSSGLDWTMT 1699
QY 1686 MNEKFMANPEPKLYEPIVTTTRKKEEEOGAAVIQRAYRKH 1728
Db 1700 MNEKFMANPEPKLYEPIVTTTRKKEEEOGAAVIQRAYRKH 1742

RESULT 13

I51964

sodium channel alpha chain SCN4A, skeletal muscle - human

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 20-Aug-1999

C:Accession: I51964

R:George, A.L.

Ann. Neurol. 31, 131-137, 1992

A:Title: Primary structure of the adult human skeletal muscle voltage-dependent sodi

A:Reference number: I51964; MUID:92246457

A:Accession: I51964

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1836 <RES>

A:CROSS-references: GB:L04236; NID:g292485; PIDN:AA59624.1; PID:g292487

C:Genetics:

A:Gene: GDB:SCN4A

A:CROSS-references: GDB:125181; OMIM:170500

A:Map position: 17q23.1-17q25.3

A:Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 536/1; 615/

C:Superfamily: sodium channel protein

C:Keywords: duplication; skeletal muscle

Query Match 47.4%; Score 4347.5; DB 2; Length 1836;

Best Local Similarity 49.2%; Pred. No. 4.3e-315;

Matches 906; Conservative 272; Mismatches 416; Indels 249; Gaps 35;

Qy 17 RPFTSDSLAAIKKRIATQKERR--KSKDKAAAEQPRPQLDLKASRKLKPLKLYGDIPELV 74
Dy 18 RPFTRESLAALEQR-AVEEEARLQNKOMETEERPERKPSRDLKAGNPLMIYGDPPPEVI 76
Qy 75 TKPLEDLPYKDKHTFWNLKKTITVRFSAKRALFTLGPENPLRSLMIRISVHSVSMF 134
Dy 77 GIPLEDLPYVSNKTTIVLKNKAIFRSATPALYLLSPESVVRGAIKVILHALFSMF 136
Qy 135 IICVTIINCFMANSMERSFNDIPEYVFIGIYILEAVIKILARGFIVDEFSLRDPNNW 194
Dy 137 IMITILNCVMTSDPPPSKNV-EYFTGIYTFESLIKILARGFCVDDFTFLRDPNNW 195
Qy 195 LDFIVIGTATCPGSGQVNLALRFRFRALKAISVIGLKIVIGALLRSVKKLVDVM 254
Dy 196 LDFSVIMAYLTERV-DLGNISALRFRVLRAKLTITVPLKLTIVGALIQSVKLSLSDVM 254
Qy 255 VLTFLCLISFALVCOQLFMGLNOKCKIKHNGCPNPASN----- 292
Dy 255 ILTVCLSVFALVGLQLFMGLNLRQKVR---WPPPFNDTNTWYSNDTWYGNEM 311
Qy 293 -----KDCFEKE-----KDSBDFIMCGTWLGRPCPN 319
Dy 312 WYGNDSHWANDTNSHASWATNDTDFDWDAYISDEGNYFFLEGSNDALLCGNSDAGHCPCQ 371
Qy 320 GSTCDKTTLPNDNNTKDFNGSWFLAMFRVMTQDSWERLYRQLRTSGIYFVFFVVVI 379
Dy 372 GYECIKTRPNYCYTSDYTFSWAFLALFLMTQDYWENLFLRAAGKTYMIFVVII 431
Qy 380 FLGSFYLLNLTLAVTWAYEQNRNVAATEAKEMFQEAQOOLRBEKEALVANGIDRSS 439
Dy 432 FLGSFYLLNLTLAVTWAYEQNRNVAATEAKEMFQEAQOOLRBEKEALVANGIDRSS 439
Qy 440 LNSLQASSFSPPKKRKFSGSKTRKSFEMRGSKTAQA---SASDSDEDDASKNPQLLEQTKRL 496
Dy 483 -----EKAAQAALGEGEADGDPHAGKCKNGCSLDTSQG 515
Qy 497 SQNLPLVDLDEHVDPLHRQRALSAYSILITITIQEOKFQEPFCPCGNKLASKYLVWDGSP 556
Dy 516 EKGAP-----RQSGSGDSGISDAMEELEAHQKCPWYKCAHKVLIWNCCA 562
Qy 557 QWLCIKKVLRTIMTDPTELAITTCIINTVFLAVEHHNMDDNLKTLKIGNWFTGTIFI 616
Dy 563 PWLFKNIHILVMDPFDVIGITTCIINTLTFMAMEHYPMTEHFDNVLTVGNLVTGTIFT 622
Qy 617 AEMCLKIATLDPHYFRHGNWVDSIVALLSLADY-LYNTLSNDRSFLASLRLVRPKL 675
Dy 623 AEWLKLIAADPHYFQOGWNIFDSIIVTSLVELGLANV---OGLSVLRSLRLVRPKL 679
Qy 676 AKSWPTLNTLKIIHSHVSGALNLTIVVITVIFSVGMRLFGTKFNK-TAYATQERPR 734
Dy 680 AKSWPTLNLKIIIGNSVAGLNLTLVLAIVFIVAVVGMQLFGSKYKCYCKTALDCNL 739
Qy 735 RWHMDNFYSLVVFVFRILCEWENTENMWGMQMDGSPCLTIIVFLVIMVIGKLVVNLFI 794
Dy 740 PRWHMDFHFLVFRILCEWENTENMWGMQMDGSPCLTIIVFLVIMVIGKLVVNLFI 798
Qy 795 ALLNLSFNE-----EKDGSLEGETRKTQVOLALDRPRRAFSE-----MLHALQSPCC 842
Dy 799 ALLNLSFNE-----EKDGSLEGETRKTQVOLALDRPRRAFSE-----MLHALQSPCC 842
Qy 843 KKCRRRKSPKPTTESF-----AGENKDSILDPAR--PWKE---YDFDMLYITGOA 889
Dy 847 -----KTLSPKDIKLSIGADGAGEGETAPEDEKKEPPEDEKKNHILNHWGLA 900
Qy 890 GAP-----LAPLAEVDDVEYCGEGALPTSQHSAGVQAGDLPPEP 930
Dy 901 DGPPSSLELDHLNFINNPLYTIQVPIASESDLE-----MPTEE-----ET 941
Qy 931 KQLTSPDQGVMEVFSEEDHLHSIQSPRKSDAVSMLESTCTDLNDIFRNLOKTV--S 988
Dy 942 DTFSEPED-----SKPPQPLYDGN--SVCSTADYKPPPEDEPEQABEN 984

Qy 989 PK-KOPDRCPKGLSCHFLCHKTKDKRSPWVLMNIRKTCYOIVKHWSFESFIIFVILLS 1047
Dy 985 PEGEQPEBCEFTACQVORWPCLYVDISQGRKKKWTTLRRACFKIVEHNNFETIFVFMILLS 1044
Qy 1048 SGALIFEDVNLPSRPOVEKLLRCDTNIPTFIFLLEMLKWAFAFGFRFTSNACWLDLEI 1107
Dy 1045 SGALAFEDIYTEQRRVIRTILEYADKVFTYIFIMEMLLKWYAGFKVFTNACWLDLEI 1104
Qy 1108 VVWSVLSLM-----NLPSLKSEFTLRALPLRALSQFEGMKVVVYALISAIPAILNVL 1160
Dy 1105 VDSIISLVANWGLVSELGPIKSLFTLRALPLRALSQFEGMRVVRVVKLLGALSIIMNL 1164
Qy 1161 LVCLIFLVFCILGVNLFSGKRCINGCTDINMYLDFTEVPPNRSC-----NISNSWKP 1216
Dy 1165 LVCLIFLVFISMGVNLFGAGFYVCINTTSERF-DISEVNNKSCESLMHTGOVRWLN 1223
Qy 1217 QVNEQNVGNAYLALLQVATYKWLJEIMNAADVDSREKQPOPEANLYAYLVFVPIIFGS 1276
Dy 1224 KVNVDNVLGLVSLLOVATFGWMDIMYAAVDSREKQPOPEANLYAYLVFVPIIFGS 1283
Qy 1277 FFTNLFTGVLIIDNFNOOKKLLGGDIFEMTEEQKYYNAMKLGTKKPKQKPIPRPLNCKQ 1336
Dy 1284 FFTNLFTGVLIIDNFNOOKKLLGGDIFEMTEEQKYYNAMKLGSKKPKQKPIPRPQNKIQ 1343
Qy 1337 AFVEDLVTQVDFVLIILGLIVLNIIMMAESADQPKDKVKTDFIL---NIAFWVIFTIEC 1393
Dy 1344 GMVYDLVTQAFDITIMILICLNMVMTMVEDDQS---QLKVDILYINIMFIIFTGEC 1400
Qy 1394 LIKVPALROHFTNGWNLFCVWVVSIIISLVSRLSDSDISFPPTLFRVVRVLARIGRL 1453
Dy 1401 VLKMLARQYFTVGNVIFDFVWVVSIIISLVSRLSDSDISFPPTLFRVVRVLARIGRL 1459
Qy 1454 RLVRAARGIRTLFALMMSLPSLNFILGLLFLVFMFIYAFGMSPKSVKKGSGIDDIENF 1513
Dy 1460 RLIRGAKIRILLFALMMSLPSLNFILGLLFLVFMFIYAFGMSPKSVKKGSGIDDIENF 1519
Qy 1514 EFTGSMCLFQITTSAGWDTLLNPMLEA-----KEHCNSSQSDSCQOQIAVVFV 1565
Dy 1520 EFTGSMCLFQITTSAGWDTLLNPMLEA-----KEHCNSSQSDSCQOQIAVVFV 1565
Qy 1566 SYIIISFLVYNNYIAVLENFNTATESEDPGLGDEDFEIFYEWEKFDPEASQIQISA 1625
Dy 1580 SYIIISFLVYNNYIAVLENFNTATESEDPGLGDEDFEIFYEWEKFDPEASQIQISA 1639
Qy 1626 LSDPADALPELPRVAKPNKQFLVMDLPMVMDRLHCHMDVLFATVTVLGDSSGDLTKT 1685
Dy 1640 LSDFVDTLOEPLRTAKPNKIKLITLDLPMVPGDKIHLCDLILFALTKVGLSGDGMALKQ 1699
Qy 1686 MMEKFMENANPKLYEPIVTTTKRKEEEOGAAYIQRAYRKH 1728
Dy 1700 TMEKFMENANPKLYEPIVTTTKRKEEEOGAAYIQRAYRKH 1728

RESULT 14

J05648

Sodium channel alpha chain - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

C:Accession: J05648; A42099

R:Wang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hoffmann, E.P. Biochem. Biophys. Res. Commun. 182, 794-801, 1992

A:Title: Sequence and genomic structure of the human adult skeletal muscle sodium ch

A:Reference number: J05648; MUID:92134303

A:Accession: J05648

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1836 <WAS>

A:Note: 861-Asp was also found as the result of polymorphism

R:McClatchey, A.I.; Van den Bergh, P.; Pericak-Vance, M.A.; Raskind, W.; Verellen, C.

Cell 68, 769-774, 1992

A:Title: Temperature-sensitive mutations in the III-IV cytoplasmic loop region of th

A:Reference number: A42099; MUID:92154689

A:Accession: A42099


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Db 1284 FFFTLNLFVGIIDNFNOQKKK--GKDI FMT EEQKYYNAMKLGSKKPKQKIPRPQNKIQ 1342
Qy 1337 AFVDELVTQSVQFVDTIILGLIVLNMIMMAESADOPKDVKTFDIL---NIAFVVIETJEC 1393
Db 1343 GMYVDLVTQKQAFDTIMILICLNVMVTMVFETDNQS---QLKVDILYNINMIFIIIFTGEC 1399
Qy 1394 LIKVPALRQHYFTNGWNLFDCVWVVLSTIISTLVSRLESDISFPPTLFRVVRLARIGRIL 1453
Db 1400 VLKMLALRQYVFTVGWNIFDFVWVILSIVGLALSGLIQK-YFVSPTLFRVIRLARIGRVL 1458
Qy 1454 RLVRARIGIRTLLEFALMMSLPSLENIGLLLEFLVMFYIAFGMSWFSKVYKSGGIDDI FNF 1513
Db 1459 RLIRGAKGIRTLLEFALMMSLPALENIGLLLEFLVMFYISIFGMSNFAYVYKESGIDDMENF 1518
Qy 1514 ETFTGSMCLCFQITTSAGWDFTLLNPMLEA-----KEHCNSSSSQDSQQPOQIAYVYFV 1565
Db 1519 ETFGNSIIICLFETTSAGWDGLLNPILNSGPPDCDPNLENPGTSVKGDCGNPSIGICEFC 1578
Qy 1566 SYIIISFLIVVMYIAVILENFNTATESEDPGLGEDDFEIEYEWKEDPEASOFIOYSA 1625
Db 1579 SYIIISFLIVVMYIAIILENFNVATESESEPLGEDDFEMFYETWEKEDPDATQFIAYSR 1638
Qy 1626 LSDFADALPEPLRVAKPNKFQFLVNDLPMVMGDRLHCMVILFAFTTRVYLGDSGSLDTMKT 1685
Db 1639 LSDFVDTLQEPRLRIAKPNKIKLITLDLPMVPGDKIHCILDLFALTKEVLGDSGEMDALKQ 1698
Qy 1686 MNEEKFEANFPKLYEPVITTTTKRKEEQGAAVIQRAYRKHM 1728
Db 1699 TMEKFMMAANPSKVSIEPITTTLRKKHHEVCAIKIQRAYRRHL 1741
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Search completed: February 27, 2002, 01:30:22
Job time: 9627 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2002, 01:29:01 ; Search time 67.45 Seconds
(without alignments)
959.428 Million cell updates/sec

Title: US-09-646-224A-2

Perfect score: 9173

Sequence: 1 MEERYYPVFPDERNRPPT.....VFCNGDLSLDVAKVKVHND 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4711.5	51.4	2016	1	CIN5_HUMAN
3	4502	49.1	2005	1	CIN2_HUMAN
4	4496.5	49.0	1951	1	CIN3_RAT
5	4496	49.0	2009	1	CIN1_HUMAN
6	4493.5	49.0	1951	1	CIN3_HUMAN
7	4484.5	48.9	2005	1	CIN2_RAT
8	4476	48.8	2009	1	CIN1_RAT
9	4363.5	47.6	1840	1	CIN4_RAT
10	4347.5	47.4	1836	1	CIN4_HUMAN
11	3983	43.4	1820	1	CIN4_ELEEL
12	3524.5	38.4	2131	1	CIN4_DROME
13	3184	34.7	1682	1	CIN6_HUMAN
14	2945	32.1	1522	1	CIN1_LOLEL
15	1508.5	16.4	1687	1	CCAM_MUSDO
16	1497.5	16.3	1873	1	CCAS_RABIT
17	1496	16.3	1873	1	CCAS_HUMAN
18	1482	16.2	2190	1	CCAD_CHICK
19	1481	16.1	2203	1	CCAD_RAT
20	1478	16.1	1835	1	CCAI_RAT
21	1475.5	16.1	1610	1	CCAD_MESAU
22	1473	16.1	2139	1	CCAC_MOUSE
23	1472	16.0	2161	1	CCAD_HUMAN
24	1469	16.0	2221	1	CCAC_HUMAN
25	1460	15.9	1852	1	CCAS_CYPCA
26	1456	15.9	2171	1	CCAS_RABIT
27	1453	15.8	2212	1	CCAA_RAT
28	1452	15.8	2326	1	CCAB_DISOM
29	1448.5	15.8	2169	1	CCAC_RAT
30	1443	15.7	2516	1	CCAD_DROME
31	1439.5	15.7	1966	1	CCAF_HUMAN
32	1438	15.7	2272	1	CCAE_MOUSE
33	1437.5	15.7	2223	1	CCAE_DISOM

34	1437	15.7	2164	1	CCAA_MOUSE
35	1434.5	15.6	2222	1	CCAE_RAT
36	1431	15.6	2353	1	CCAH_HUMAN
37	1430.5	15.6	2312	1	CCAE_HUMAN
38	1426.5	15.6	2339	1	CCAB_RABIT
39	1422.5	15.5	2254	1	CCAG_RAT
40	1421	15.5	2259	1	CCAE_RABIT
41	1412	15.4	2339	1	CCAB_HUMAN
42	1407	15.3	2336	1	CCAB_RAT
43	1405	15.3	2424	1	CCAA_RABIT
44	1404.5	15.3	2505	1	CCAA_HUMAN
45	1402	15.3	2377	1	CCAG_HUMAN

ALIGNMENTS

RESULT 1
CIN5_RAT
AC P15389; STANDARD; PRT; 2019 AA.
DT 01-APR-1990 (Rel. 14, Created)
ET 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SODIUM CHANNEL PROTEIN, CARDIAC MUSCLE ALPHA-SUBUNIT.
GN SCN5A.
QS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
FN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=90046760; PubMed=2554302;
RA Rogart R.B., Cribbs L.L., Muglia L.K., Kephart D.D., Kaiser M.W.;
RT "Molecular cloning of a putative tetrodotoxin-resistant rat heart Na+
channel isoform.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8170-8174(1989).
CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT. IT IS A TETRODOTOXIN-RESISTANT NA+ CHANNEL ISOFORM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
CC -!- MISCELLANEOUS: NA+ CHANNELS IN MAMMALIAN CARDIAC MEMBRANE HAVE
FUNCTIONAL PROPERTIES QUITE DISTINCT FROM NA+ CHANNELS IN NERVE
AND SKELETAL MUSCLE.
CC -!- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL; M27902; AAA42114.1; -;
CC PIR; A33996; A33996.
CC InterPro; IPR002111; Cat_channel_TrpL.
CC InterPro; IPR000636; Cation_chan_non_lig.
CC InterPro; IPR001682; Channel_pore_Ca_Na.
CC InterPro; IPR000048; IO.
CC InterPro; IPR001696; Na_channel.
CC Pfam; PF00520; ion_trans; 4.
CC Pfam; PF00612; IQ; 1.
CC PRINTS; PR00170; NACHANNEL.

Db 898 VGMQLFGSKYKCEVCCKISNDCELP--RWHMDFHPSFLVFRVLCGEWETMWDCCM-EVA 954
Qy 770 GSPCLIIIVFVIMVIGKVLNLFALLNLSFNEKDGSGLEGETRKTQVOLALDRPFRRA 829
Db 955 GQTHCLTVFMVWVIGNVLVNLFLALLSSESSDNL-AAVDDDDNEMNQLIAGVRMKG 1013
Qy 830 FSEMLHALQSCCKCRKRKNSP---KPKETTESPAGENKDSILDPARPKREYDPTDMALY 885
Db 1014 IDFKVRKTRFQKAFVRKQKALDEIKPLEDLNN---KQSCISN----- 1055
Qy 886 TQGAGAPLAPAEVDDVEYCEGEG---GALPTSQHSAGVQAGD---LPPETKOLTSF- 936
Db 1056 -----HTTETGKDLNLYKDGNGTTSIGGSSVYKVVDESPTMFINPSLTVTVP 1107
Qy 937 -----DDGQVEMEVFSEDLHLISQSPRKKSDAVSMLSECTSIDLNDIFRNLOKTVSPKK 991
Db 1108 AVGESDFENLNTERRSSES---DWEESKEKLNATSS-SEGSTVDIGAPAEQEPVEPEE 1163
Qy 992 ---QDRCFPKGLSCHFLCHKTKDKRSPWVLMNIRKTCYQIVKHSWFESFIIFVILLSSG 1049
Db 1164 SLEPEACFTEDCVRKFKCCQISIEBGKGLKWNLRKTKCYKIVHNWFTFIVEMILLSSG 1223
Qy 1050 ALIFEDVNLPSRPOVEKILRCTDNIFTIFILLEMILKWAQVGRFYFTSANCWLDFLIV 1109
Db 1224 ALAFEDIYEQRTIKTLMLEYADKVFYTFIFILEMLKWAQVGFYFTNACWLDFLIVD 1283
Qy 1110 VSVLSL-----MNLPSLKFRTLRALRPLRALSOFSGKVVVYVYALISAIPAILNVLV 1162
Db 1284 VSLVSLTANALGYSELGAIKSURLRALRPLRALSFRGMRVAVNALGALPSIMNVLV 1343
Qy 1163 CLIFLWVFCILGVNLFSKFGRCINGTDINMYLDFTEVFNRSQCN-----SNYS--WKVPQ 1217
Db 1344 CLIFLWVFCILGVNLFSKFGRCINGTDINMYLDFTEVFNRSQCN-----SNYS--WKVPQ 1402
Qy 1218 VNFDMVGNAYLALQVARYKQWLEIMNAAVDSREKDEQDPDEANLYAVLYFVFIIFGSF 1277
Db 1403 VNFDMVGNAYLALQVARYKQWLEIMNAAVDSREKDEQDPDEANLYAVLYFVFIIFGSF 1462
Qy 1278 FTNLNLFVIGVINDFNQOQKLGQDIFMTEQKYYNNAKMLGTGKPKPPIRPLNKKQA 1337
Db 1463 FTNLNLFVIGVINDFNQOQKLGQDIFMTEQKYYNNAKMLGTGKPKPPIRPLNKKQA 1522
Qy 1338 FVFDLVTSQVDFVILGLVILNMIMMAESADQPKDKKTKFDILNIAFVFIIFGLIKV 1397
Db 1523 MVFDFVTKQVDFISIMILICLNMVMTVETDDQSQEMNILYWINLVFLVFTGECVLK 1582
Qy 1398 FALROHYFTGNLFDCCVVLVLSIISTLVSR-EDSDISFPPTLFRVRLARIGRILRV 1456
Db 1583 ISLRYVYFTGNVIFDFVVLVLSIISVGMFLAELIEKYFVS--PTLFRVRLARIGRILRV 1640
Qy 1457 RAARGIRTLFALMMSLPSLNFIGNLGLLFLVMFVIAIFGMSWFSKVKKGSGIDDIENFETF 1516
Db 1641 KGAKGIRTLFALMMSLPSLNFIGNLGLLFLVMFVIAIFGMSWFSKVKKGSGIDDIENFETF 1700
Qy 1517 TGSMLCLFQITTSAGWDTLNPLMEA-----KEHCNSSQSDSCQOQPIAVVYFVS 1568
Db 1701 GNSMCLFQITTSAGWDTLNPLMEA-----KEHCNSSQSDSCQOQPIAVVYFVS 1760
Qy 1569 IISFLVVMNYIAVILENFATNATESDEPDLGEDDEIFEYEWKEDPEASQFIQYALSAD 1628
Db 1761 IISFLVVMNYIAVILENFATNATESDEPDLGEDDEIFEYEWKEDPEASQFIQYALSAD 1820
Qy 1629 FADALPELRVAKPNKQFVLMVMDLPMWMDRHLCHMDVLFAPFTTRVLDGSSGLDWTWME 1688
Db 1821 FADALPELRVAKPNKQFVLMVMDLPMWMDRHLCHMDVLFAPFTTRVLDGSSGLDWTWME 1880
Qy 1689 EKFMANPKFKLYEPIVTTTRKEEEOGAQVIAQRYKHM-----EKMKVLRKLRDSSSS 1743
Db 1881 ERFMASNPKSKVSEPIVTTTRKEEEOGAQVIAQRYKHM-----EKMKVLRKLRDSSSS 1939
Qy 1744 HQVFCNG 1750
I: I

Db 1940 ----CDG 1942
RESULT 4
CIN3_RAT STANDARD; PRT: 1951 AA.
XO CIN3_RAT
AC P08104;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SODIUM CHANNEL PROTEIN, BRAIN III ALPHA SUBUNIT (VOLTAGE-GATED SODIUM CHANNEL SUBTYPE III).
DE SCN3A.
GN SCN3A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX [1]
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=88137594; PubMed=2449363;
RA Kavano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
RT "Primary structure of rat brain sodium channel III deduced from the cDNA sequence.";
RL FEBS Lett. 228:187-194(1988).
CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -!- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -!- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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CC EMBL; Y00766; CAA68735.1; -
DR PIR; S00320; S00320.
DR InterPro; IPR002111; Cat_channel_trpl.
DR InterPro; IPR000636; Catlon_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ_1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00015; IQ; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Repeat; Multigene family.
FT TRANSMEM 124 147 S1 OF REPEAT I.
FT TRANSMEM 156 175 S2 OF REPEAT I.
FT TRANSMEM 189 207 S3 OF REPEAT I.
FT TRANSMEM 214 233 S4 OF REPEAT I.
FT TRANSMEM 249 273 S5 OF REPEAT I.
FT TRANSMEM 401 426 S6 OF REPEAT I.
FT TRANSMEM 706 730 S1 OF REPEAT II.
FT TRANSMEM 742 765 S2 OF REPEAT II.
FT TRANSMEM 774 793 S3 OF REPEAT II.
FT TRANSMEM 800 820 S4 OF REPEAT II.

FT TRANSMEM 836 856 S5 OF REPEAT II.
 FT TRANSMEM 910 935 S6 OF REPEAT II.
 FT TRANSMEM 1153 1176 S1 OF REPEAT III.
 FT TRANSMEM 1190 1215 S2 OF REPEAT III.
 FT TRANSMEM 1222 1243 S3 OF REPEAT III.
 FT TRANSMEM 1248 1269 S4 OF REPEAT III.
 FT TRANSMEM 1289 1310 S5 OF REPEAT III.
 FT TRANSMEM 1393 1419 S6 OF REPEAT III.
 FT TRANSMEM 1473 1496 S1 OF REPEAT IV.
 FT TRANSMEM 1508 1531 S2 OF REPEAT IV.
 FT TRANSMEM 1538 1561 S3 OF REPEAT IV.
 FT TRANSMEM 1572 1593 S4 OF REPEAT IV.
 FT TRANSMEM 1609 1631 S5 OF REPEAT IV.
 FT TRANSMEM 1698 1722 S6 OF REPEAT IV.
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 835 835 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1002 1002 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1019 1019 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1331 1331 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 1951 AA: 221385 MW: 745E851524BD10E CRC64;

Query Match 49.0%; Score 4496.5; DB 1; Length 1951;
 Best Local Similarity 49.0%; Pred. No. 3e-277;
 Matches 945; Conservative 282; Mismatches 444; Indels 257; Gaps 36;

Qy 11 PDERNFRPFTSDSLAAIKRIAIQERKKSKD-AAAPQPPQRLDQKASRLKPLKLYGDI 69
 Db 9 PGPESEFLUTRESLAAIEKRAAEERAKKPKKEQDIDENKPKNSDLEAGNLPFIYGD 68
 Qy 70 PPELVTKPLEDDPYVYKHKTFWLUNKRTYRFSAKRALFTLGFNPNPLRSLMTRISVHS 129
 Db 69 PPEMVSEPLEDDPYVYVSKKTFVVLUNKKAIFRFSATSALYILTLPLNPKVIAIKILVHS 128
 Qy 130 VFSMFIICITVINCMANSMERSFDNDIPEVVFVIGVILEAVIKILARGFTVDFEFLR 189
 Db 129 LFSMLIMCITLNCVFMFLSNPPDKNV-EYTFGFIYFESLILKILARGCELDFTFLR 187
 Qy 190 DPWNMLDFVIGTATATCPGSOVNLALRTFRFRALKALISVISGLKVIIVGALLRSYKK 249
 Db 188 DPWNMLDFSVIMAYVTEV-DLGNVSALRTFRVLRLAKLTISVIPGLTIVGALLIQSYKK 246
 Qy 250 LVDVWVLTLFCLSLFALYGOQLFMGILNOKIKHNCGNPNASNKDCPFKEKDS----- 302
 Db 247 LSDVMILTAVFLCSVPEALIGLOLMGNLRNKSQW-----PPSD-SAFETNTTSYFNGTMD 300
 Qy 303 -----EDFTMCGTWLGSRPCNGSCTDKTLNPD 331
 Db 301 SNGTFVNTMTFNKWDYIADDSHPYVLDGQKDPDLCNGSDAGOCPEGYICVKAAGRPN 360
 Qy 332 NNYTKDFNGSFLAMFRVMTQDSWERLYRQLRTSGTYFFVFFVWVIFLGSFYLLNLTL 391
 Db 361 YGYTSDFDTSWAFSLFLRLMTQDYENLYQLTLRAAGKTYMFFVLVIFLGSFYLVNLIL 420
 Qy 392 AVVTMAYEQNRNVAETEAKEMFQEAQQLLREPEKALVAM-----GIDR 437
 Db 421 AVVAMAYEQNAATLEEAQEAQEAQFQOQLKQOEAQAAVAAAASARSDFSGIGGLGE 480
 Qy 438 SSLSLQASSFPSPKKEFFGS---KTRKSEFMRSKTAQAS---ASDSEDAASK----- 485
 Db 481 LLESSEASKLSSKSAKEWRNRKRQRHLEHGRHNRADGRFPKSESEDSVKRRSFLLS 540
 Qy 486 ---NPQLEOKTRL-----SQNLVDLDF-----DEH 508
 Db 541 LDGNP--LJGDKKLCSPHQSLLSIRGSLFSPRNSKTSIFRGRKADVGSENDPADDEH 598

509 -----VDPHQRALS 519
 599 STFESESRDLSLPHRPGERRNSGTTTETEVKRRLSSQYISMEWLESSGQRMS 658
 520 AVSILITIQOEKFOEPCPGKNLASKYLWDCSPWLCKIKVLRITMDPFFELAIT 579
 659 IASILTNTMELEESRQKPCPCWYRFANVFLWDCDARLKVHLNVLVMDPFFDLAIT 718
 580 ICIIINTVFLAVEHHNMDNLKILKIGNVFTGIFIAEMCLKIIALDPHYFRHWNVF 639
 719 ICIVLNTLFMAHEHPMTQOESSVLTVGNLVTGIFTAEVLIKIAMDPIYVYFQEGWIF 778
 640 DSIIVALLSLADV-LYNTLSDNRRSPLASLRVLRVFKLAKSWPTLTLIKIGHSVGALGN 698
 779 DGIIVLSLMEIGLANV---EGLSVLRSFRLLRVFKLAKSWPTLNLMLKIIGNSVAGALN 835
 699 LTVLTVIVVFISVVGMLFGTKPK-K-TAYATQERPRRRWMDNFYHSLFVVRILCGEW 757
 836 LTLVLAIVFVAVVGMOLFCKSYKECVCKINVDCKLPRWMDNFHSLFVVRILCGEW 895
 758 TENMGMQDDGSPCLIIIVFLIMVIGLVNLFIALLLNSFNEEKDGSLGETRKT 817
 896 IETMWDKM-EVAGQTMCLIVMLVIGNLVNLFALLLSFSSDNL-AATDODNEMN 953
 818 KVQALDRFRRAFSFMLHALQSFCCKKCRK---NSPKPKETTESFAGENKDSILLDARP 874
 954 NLOIIVGRMKGIDFVNKKI-----RECRAFFRKPVIETQEG----- 993
 875 WKEDTDMLTYTGOAGAPLAEVEDDVEYCGEGALPTSOHSAGVAGO----- 925
 994 -NKIDSCMSNNTG-----IEISKELNYLKDNGT-----TSGVTGSSVEKYVIDE 1038
 926 -----LPEPTKQLTSP-----DDQGVEMEVFSEEDLHLSIQSPRKKSADVSMISEGT 973
 1039 NDYMSFINNPSLTVTVPITAVGESDFENLTBEFSSES---ELEESKEKLNATSS-SEGST 1094
 974 IDLNDIFRNLOKTVSPKK--OPDRCPFKGLSCHFCHTKDRKSPWLWNRKTCYQIV 1031
 1095 VDVAPPREGEOAEIEPEDLKAPEACFEGCCKKFPFCQVSTBEGKGTWNLNRTKCYSTIV 1154
 1032 KHSNPESFIIFVILLSSGALIFEDVNLSPQVEKLLACTONITFTIFLEMLLKWAVG 1091
 1155 EHNFEFTIVFIMLSSGALAFEDIYIEQRTIKTMEYADKVFTYIFILEMLLKWAVG 1214
 1092 FRRYTSAMCWLDLIVVSVLSL-----NLPSLSFRTRLRALRPLRALSQPEGMKV 1144
 1215 FQYFTNACWMLDPLVDVSLVSLVANALGYSELGAIKSLRTRLRALRPLRALSREGMV 1274
 1145 VYVALISAIPAILNVLVCLIFVFLVFCILGVNLFSKFGRCINGTDINMYLDFTEVPNRS 1204
 1275 VVNALVGAIPSIMNVLLVCLIFVFLVFSIMGNVLFAGKYHCVTNTTGNMF-EIKEVNNFS 1333
 1205 OCNI--SNYSKMPVOPNFNDVGNVYALLOVATYKGLWLEIMNAADVDSREKDEOPFENL 1262
 1334 DQCALGKQARKNVKNVFNFDNVGAGYALLOVATFGWMDIMYAAVDSRDXKLQPIYENL 1393
 1263 YAYLVFVFIIFGSPFTLNLFIIDNFNOQKKGGLGQIDFMTBEQKKYNNAMKLGTK 1322
 1394 YMYLVFVFIIFGSPFTLNLFIIDNFNOQKKGGLGQIDFMTBEQKKYNNAMKLGSK 1453
 1323 KPQRPRLPLNKCQAFVFDLTVSQVFDVITLGLIVNMIIMAESADQPKVKKFTDILN 1382
 1454 KPQKPIPRANKFGQWDFVTRQVFDISIMILICLNMTVMVFDDQSKYMTLVLIRN 1513
 1383 IAFVVFITECLIKVFAIRQHYETNGWNLFDCCVVVVLSTISFLVSL-EDSDISFPPTLF 1441
 1514 LVFVILTFGEFLKLISURYYIFTIGNWIFDFVWVILSVGMFLAELEKIFVS--PTLF 1571
 1442 RVVRLARIGRILRVRAARGITRLFLALMMSLPSLNFILGLLFLVYMFYIATFGMSWFSK 1501
 1572 RVIRLARIGRILRLIKAGKIGITRLFLALMMSLPALFNIGLGLLFLVYMFYIATFGMSFAV 1631

-1- DISEASE: DEFECTS IN SCN1A ARE THE CAUSE OF GENERALIZED EPILEPSY WITH FEBRILE SEIZURE PLUS TYPE 2 (GEFS-2). THIS AUTOSOMAL DOMINANT DISORDER IS CHARACTERIZED BY FEBRILE SEIZURES IN CHILDREN AND AFBRIE SEIZURES IN ADULTS. PENETRANCE IS INCOMPLETE AND A LARGE INTRAFAMILIAL VARIABILITY OF THE PHENOTYPE IS OBSERVED.

-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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EMBL: S71446; AAB31605.1; --
EMBL: X65362; CRA46439.1; --
EMBL: M91803; --; NOT_ANNOTATED_CDS.
PIR: S29184; S29184.
MIM: 182389; --
MIM: 604233; --
InterPro: IPR002111; Cat_channel_TrpL.
InterPro: IPR000636; Cation_chan_non_lig.
InterPro: IPR001682; Channel_pore_Ca_Na.
InterPro: IPR000048; IQ.
InterPro: IPR001696; Na_channel.
Pfam: PF00520; Ion_trans; 4.
Pfam: PF00612; IQ; 2.
SMART: SM00015; IQ; 1.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Glycoprotein; Repeat; Multigene family; Disease mutation.
REPEAT 110 454
I (BY SIMILARITY).
REPEAT 750 1022
II (BY SIMILARITY).
REPEAT 1200 1514
III (BY SIMILARITY).
REPEAT 1523 1821
IV (BY SIMILARITY).
TRANSMEM 124 147
S1 OF REPEAT I (BY SIMILARITY).
TRANSMEM 156 175
S2 OF REPEAT I (BY SIMILARITY).
TRANSMEM 189 207
S3 OF REPEAT I (BY SIMILARITY).
TRANSMEM 214 233
S4 OF REPEAT I (BY SIMILARITY).
TRANSMEM 250 273
S5 OF REPEAT I (BY SIMILARITY).
TRANSMEM 400 425
S6 OF REPEAT I (BY SIMILARITY).
TRANSMEM 763 787
S1 OF REPEAT II (BY SIMILARITY).
TRANSMEM 799 822
S2 OF REPEAT II (BY SIMILARITY).
TRANSMEM 831 850
S3 OF REPEAT II (BY SIMILARITY).
TRANSMEM 857 876
S4 OF REPEAT II (BY SIMILARITY).
TRANSMEM 893 913
S5 OF REPEAT II (BY SIMILARITY).
TRANSMEM 967 992
S6 OF REPEAT II (BY SIMILARITY).
TRANSMEM 1214 1237
S1 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1251 1276
S2 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1283 1304
S3 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1309 1330
S4 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1350 1377
S5 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1457 1483
S6 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1537 1560
S1 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1572 1595
S2 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1602 1625
S3 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1636 1657
S4 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1673 1695
S5 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1762 1786
S6 OF REPEAT IV (BY SIMILARITY).
CARBOHYD 211 211
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 284 284
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 295 295
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 301 301
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 306 306
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 338 338
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 601 601
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 621 621
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 681 681
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 892 892
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 1064 1064
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 1080 1080
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 1146 1146
N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1378 1378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1392 1392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1403 1403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1788 1788 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 875 875 T -> M (IN GEFS+2).
FT VARIANT 1648 1648 /FTId=VAR_010110.
FT VARIANT 1537 1537 R -> H (IN GEFS+2).
FT CONFLICT 1537 1537 /FTId=VAR_010111.
FT CONFLICT 1537 1537 F -> L (IN REF. 3).
SQ SEQUENCE 2009 AA; 228970 MW; 0593A6730F33C9A2 CRC64;

Query Match 49.0%; Score 4496; DB 1; Length 2009;
Best Local Similarity 47.8%; Pred. No. 3.3e-277;
Matches 945; Conservative 287; Mismatches 433; Indels 312; Gaps 38;

Qy 11 PDENRFRPTSDSLAAIKRIAIQERKKSKDKA-AABPQRPQDLKASRLPKLYGDI 69
Db 11 PDSFNF--FTRESLAAIERIAEAKAKPKDPKDDDDGPKPNSDLEAGKNLPIIYDI 68
Qy 70 PPELVTKPLEDLDPYKDKHFKFWLNKRTYRFSAKRALFILGPNPLRSLMIRISVHS 129
Db 69 PPEMVSEPLEDLDPYINKTKFIWLNKKAIFRSATSALYILTPFNPLRKIAIKILVHS 128
Qy 130 VFSMFICTVIINCFMANSERSDNDIPEVVFYIGVILEAVIKILARGFTIVDFSFRL 189
Db 129 LFSMLIMCTIITNCVFMTPSNPPDWTKV-EYFTGTYTFESLKIARGCLEDFTFLR 187
Qy 190 DPWNMLDFIVGTATATCPGSOVNLSALRTRFRVFRALKAI SVISGLVIVGALLRSVKK 249
Db 188 DPWNMLDFIVTFAVTEFV-DLGNVSALRTRFRVRLALKTISVIPGLKTIVGALLQSVKK 246
Qy 250 LVDVWVLTCLSPALVQOQLFMGLNOKCI-----KHNCGPN-----PASN 292
Db 247 LSDVMILTVFCLSPALVQOQLFMGLNOKCIQWPPPTNASLEHSIEKNTIVNYNGTLN 306
Qy 293 KDCFEKE-----KQSE-----DFTMCGTWLGRPCPGSTCDKTLPLDNNYTKFD 338
Db 307 ETVEFDWKS YIQDSRYHYFLEGLDALLCGNSSDAGQCPGYMCVKAGRPNVGYTSD 366
Qy 339 NFGSFLAMFRVWQDSWERLYRQILRTSGIYFVFVVFVFLGSLYLLNLT LAVVTMAY 398
Db 367 TFSWAFSLFLMTQDQWENLYQLTRAAGTKYTIFFVFLVFLGSLYLLNLT LAVVAMAY 426
Qy 399 EEQRNVAATEAKEMFOEAQQLLEKE-----ALVAMGIDRS-----438
Db 427 EEQNATLEAEAKAEFOQMEQLKQOEAQAQAATASEHSREPSAAGRLSDSSEA 486
Qy 439 -----438
Db 487 SKLSSKAKERRNRKRRKQEQSGEKEDEFEQKSESDSIRKQPRFSIEGNRLTYE 546
Qy 439 -----SLNSLQASSPSPKRRFFGSKTRKSF-MRGSKTAQASD-----SED 481
Db 547 KRYSPHOSLISIRGSLFSRPR-----NSRSLFSFRGRKRAKVGSENDADDEHSTPED 600
Qy 482 DASKNPOL-----LEOTKRLS-----497
Db 601 NESRDSLFVPRRUGERNNSLQTSRSRMLAVFPANGKMHSTVDCNGVYSLVGGPSVP 660
Qy 498 -----QNLVDFLDF-----HV-----DPLHRQALSAVSIL 524
Db 661 TSPVQQLLPEVIDKPAITDNGTTTETEMRRKRRSSSFHVSMDLEDPSPQRQAMSIASIL 720
Qy 535 TITQEQKFOBPCKGNLASKYLVWDCSPQWCIKKVLRITWDTPTTELATICILII 584
Db 721 TMTVEELERQKCPCKPYKESNIFLWDCSPYWLKVHVHVNVLVMDPFVDLAITICIVL 780
Qy 585 NTVFLAVENHNDNLKTIKIGWVFTGIFIAEMCLKIIALDPVHYFRHGNVDFDSIVA 644
Db 781 NTLFAMEHYPTDHFNNVLTVGNLVFTGIFTAEMFLKIALMDPPYIFQEGNIFDGVIV 840
Qy 645 LLSLADV-LYNTLSDNNRSFLASURLRVFVKLAKSWPTLNTLKIIGHSGVAGLNLTVVL 703

841 TLSLVELGLANV---EGLSVLSRFPLLRVFKLAKSWPTLNLMLKIIGHSGVAGLNLTVL 897
Qy 704 TIVVFISVWGMRLFGTKFN---KATAYATQERPRRRHMDNFYHSFLVFRILGGEWIE 759
Db 898 ALIIVFAVGMQLFGSKYKDCVCKIASDCQ---LPRWHMDFHSHFLVFRILGGEWIE 954
Qy 760 NWWGCMQMDGSPCLIIIVFLIWIWIKLVNLFTALLNLSFNEEKDGSLEGERTKTKV 819
Db 955 TMDCM-EVAGQAMCLTVFMVMVIGNVLNLFALLLSFSADNL-AATDDDNEMNL 1012
Qy 820 QLALDRERRAFSFMHLALQSFCCKKRRKNSPKPKETTESFAGENKSDTLDPDAREWKEY- 878
Db 1013 QIADRMHKGVAIVYKRIYEF-----IOOSFI---RKQILDEIKPLDDLN 1055
Qy 879 ---DTDMALYTOAGAPLAPLAEDVVEYCGEGAL-----PTSOHSA 919
Db 1056 NKDCSMNHATAEIGKLDYLDKDVNGTTSIGTGSSVEKYIIDESDYMSFINNPSLTVTV 1115
Qy 920 GVOAGDLPETKQLTSPDQGVEMEVFSEEDLHLSIQSPRKSDAVSMLSECSSTDLNDI 979
Db 1116 PIAVGE-----SDFENLNTEDFSSES---DLEESKEKLNESSESSEGSTVDIGAP 1162
Qy 980 FRNLQKTVSPKK--QPDRCFPKGLSCHFKHTDKRKSPWVLWNWIRKTCYQIVKHSPE 1037
Db 1163 VEE-QPVVEPETLEPEACFTGCGVQRKCCQINVEEGRGQWMLRTRTCFRIVEHNFE 1221
Qy 1038 SFIIFVILLSSGALIFEDVNLSPRQVBEKLLRCDTNIETFLLEMLKLVKAFGRRYFT 1097
Db 1222 TFIIVMILLSSGALAFDIYIDQRTIKTMLEYADKVYTFIEMLLKLVKWAYGYQYFT 1281
Qy 1098 SAWCHLDLIVVSVLSL-----MNLPSLKSFTLRALRPLRALSOFEGMKVYVYALI 1150
Db 1282 NAWCWLDLIVDVSVLSLTANALGYSELGATKSLRTRALRPLRALSFEGRVYVYVALL 1341
Qy 1151 SAIPAILNVLIVCLIFLWVFCILGVNLFSGFGRCINGT-----DINMYLDFTEPN 1202
Db 1342 CAISIMNVLLVCLIFLWVFCILGVNLFSGFGRCINGT-----DINMYLDFTEPN 1401
Qy 1203 RSQCINISYWKVQVNFNDVGNAYLALLOVATYKGLWEIMNAAVDSREKQDQDFEALN 1262
Db 1402 RNE-----TARKNKVKNFNDVNGFGLSLQVATEKGMWDIMYAAVDSRNVELQPYEESL 1457
Qy 1263 YAYLVFVFIIFGSPFTLNLFGVIIDNFNOOKKLGODIFMTEEOKKYINAMKLGTK 1322
Db 1458 YMYLFVFIIFGSPFTLNLFGVIIDNFNOOKKLGODIFMTEEOKKYINAMKLGSK 1517
Qy 1323 KPQKPIRPLAKCAVFDLVTSQVFDVILGLIVLNNMIIMAESADQPKDVKKTFDILN 1382
Db 1518 KPQKPIRPNKFGQVDFVTRQVFDISIMILICLNNVMTMVTDDQSEYVTTILSRIN 1577
Qy 1383 IAFVVIFTEGLIKVAFALRQHYFTNGWNLFDQVWVLSIISITLVSRL-EDSDISPPPLF 1441
Db 1578 LVFVLETFEGCVKLISURHYFTTIGWNIFDVVYVILSIGVFMFLAELEKTFVS--PTLF 1635
Qy 1442 RVVRLARIGRILRLVRAARGITLLFALMMSLPSLFNIGLILLFLVMFYIATFGMSWFSKV 1501
Db 1636 RVIRLARIGRILRLKAGRGITLLFALMMSLPSLFNIGLILLFLVMFYIATFGMSNFAIV 1695
Qy 1502 KKGSDIDIFNFTFTGSMCLFQITTSAGWDTLNLPMLEAK-BHCN-----SSQDS 1553
Db 1696 KREVGIDDMENFETFGSMICLFIQTTSAGWDGLLAPILNSKPPDCDPKNVPGSVKGD 1755
Qy 1554 CQQQIIVAVYFVYIIISFLIVVMYIAVILENFNTATEESEDPLGEDDFEIFYEWBKF 1613
Db 1756 CGNSVGVFFFYIIISFLVVMYIAVILENFNTATEESEDPLGEDDFEIFYEWBKF 1815
Qy 1614 DPEASQIYQSALSDADALPELRVAKPNKFOFLVMDLBVMVGDRLHMDVLFATPRV 1673
Db 1816 DPDAQFQMEFKLSQFAALEPPLNLPQNKQLQTLAMDOLPMVSGDRIHCLDLIFATPRV 1875
Qy 1674 LGDSGLDTRMTMBEEKFMEANPKKLYEPIVTTTKRKEEGQGAIVIQRAYRKHEK 1730
Db 1730 LGDSGLDTRMTMBEEKFMEANPKKLYEPIVTTTKRKEEGQGAIVIQRAYRKHEK 1730

Db 1876 LCSEGDALRIQMEERFASNPVKSVQPIITTLKRRQEVSAVIOAIRRHLLK 1932

RESULT 6

CIN3_HUMAN

ID CIN3_HUMAN STANDARD; PRT: 1951 AA.

AC O9NY46: O9Y64; Q9UPD1; Q16142; Q9NYK2;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE SODIUM CHANNEL PROTEIN, BRAIN III ALPHA SUBUNIT (VOLTAGE-GATED SODIUM CHANNEL SUBTYPE III).

DE SCN3A OR NAC3.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Chen Y., Dale T.J., Romanos M.A., Whitaker W.R., Xie X., Clare J.J.;

RT "Cloning, distribution and functional analysis of the human brain type III sodium channel from human brain.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-1366 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98251277; PubMed=9589372;

RA Lu C.M., Brown G.B.;

RT "Isolation of a human-brain sodium-channel gene encoding two isoforms of the subtype III alpha-subunit.";

RL J. Mol. Neurosci. 10:67-70(1998).

RN [3]

RP SEQUENCE OF 1275-1364 FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=94211784; PubMed=8159690;

RA Malo M.S., Srivastava K., Andresen J.M., Chen X.N., Korenberg J.R., Ingram V.M.;

RT "Targeted gene walking by low stringency polymerase chain reaction: assignment of a putative human brain sodium channel gene (SCN3A) to chromosome 2q24-31.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:2975-2979(1994).

RN [4]

RP SEQUENCE OF 1620-1701 FROM N.A.

RC TISSUE=Kidney;

RA Tonkovich G.S., Kyle J.W.;

RT "Endogenous sodium current in HEK293 cells: increase in cell surface expression of endogenous currents by stable transfection of the Beta 1 subunit.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch.

DR EMBL; AJ251507; CAB85895.1; -

DR EMBL; AF035685; AAC29514.1; -

DR EMBL; AF035686; AAC29515.1; -

DR EMBL; S69887; AAB30530.1; -

DR EMBL; AF239921; AAF44690.1; -

DR MIM; 182391; -

DR InterPro; IPR002111; Cat_channel_TrpL

DR InterPro; IPR000636; Cation_chan_non_lig

DR InterPro; IPR001682; Channel_pore_Ca_Na

DR InterPro; IPR000048; IQ

DR InterPro; IPR001696; Na_channel

DR Pfam; PF00520; Ion_trans; 4

DR Pfam; PF00612; IQ; 1

DR PRINTS; PR00170; NACHANNEL

DR SMART; SM00015; IQ; 1

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Glycoprotein; Repeat; Multigene family; Alternative splicing.

ET TRANSMEM 124 147 S1 OF REPEAT I.

ET TRANSMEM 156 175 S2 OF REPEAT I.

ET TRANSMEM 189 207 S3 OF REPEAT I.

ET TRANSMEM 214 233 S4 OF REPEAT I.

ET TRANSMEM 249 273 S5 OF REPEAT I.

ET TRANSMEM 401 426 S6 OF REPEAT I.

ET TRANSMEM 706 730 S1 OF REPEAT II.

ET TRANSMEM 742 765 S2 OF REPEAT II.

ET TRANSMEM 774 793 S3 OF REPEAT II.

ET TRANSMEM 800 820 S4 OF REPEAT II.

ET TRANSMEM 836 856 S5 OF REPEAT II.

ET TRANSMEM 910 935 S6 OF REPEAT II.

ET TRANSMEM 1153 1176 S1 OF REPEAT III.

ET TRANSMEM 1190 1215 S2 OF REPEAT III.

ET TRANSMEM 1222 1243 S3 OF REPEAT III.

ET TRANSMEM 1248 1269 S4 OF REPEAT III.

ET TRANSMEM 1289 1310 S5 OF REPEAT III.

ET TRANSMEM 1393 1419 S6 OF REPEAT III.

ET TRANSMEM 1473 1496 S1 OF REPEAT IV.

ET TRANSMEM 1508 1531 S2 OF REPEAT IV.

ET TRANSMEM 1538 1561 S3 OF REPEAT IV.

ET TRANSMEM 1572 1593 S4 OF REPEAT IV.

ET TRANSMEM 1609 1631 S5 OF REPEAT IV.

ET TRANSMEM 1698 1722 S6 OF REPEAT IV.

ET CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 835 835 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 1002 1002 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 1019 1019 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 1317 1317 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CARBOHYD 1331 1331 N-LINKED (GLCNAC. . .) (POTENTIAL)

ET CONFLICT 175 175 A -> V (IN REF. 2).

ET CONFLICT 208 208 S -> D (IN REF. 2); AAC29515).

ET CONFLICT 318 318 Y -> N (IN REF. 2).

ET CONFLICT 401 401 M -> T (IN REF. 2).

ET CONFLICT 606 606 S -> T (IN REF. 2).

ET CONFLICT 613 613 V -> E (IN REF. 2).

ET CONFLICT 1011 1011 E -> A (IN REF. 2).

ET CONFLICT 1225 1225 W -> R (IN REF. 2).

ET CONFLICT 1280 1280 V -> L (IN REF. 3).

ET CONFLICT 1365 1366 AT -> VS (IN REF. 2).

SQ SEQUENCE 1951 AA; 221459 MW; B692555143D6C8B5 CRC64;

Query Match 49.0%; Score 4493.5; DB 1; Length 1951;
Best Local Similarity 48.7%; Pred. No. 4.6e-277;

Matches 940; Conservative 294; Mismatches 452; Indels 245; Gaps 33;

QY	11	PDERNRPPTSDSLAAIKRRIAIOERKSKDK--AAAPQPPQOLDLKASRKLKPLYGDI	69
Db	9	PGPESRLEPTRESLIAEKAABEAKAKPKKQDNDENKPKNSDLBAGNKLFIYGI	68
QY	70	PPELVTKPLEDDPYKDKHTFWLWLNKKRTIYFSAKRALFLIGPENPLRSLMTRISVHS	129
Db	69	PPWVSEPLEDDPYVINKKTFIVNKKGAIFFSATSALYILTLPLNPKVIAKILVHS	128
QY	130	VFSNFICTVINCMPMANSERSDNDIPEYVFTIGVILEAVTKILARGFIVDFEPLR	189
Db	129	LFSLNIMCTILTNCPWTLNPNPDWTKV--EYTFGTIYTESLIKILARGCELEDFPLR	187
QY	190	DPNNWLDFTVIGTAIATCFPGSOVNLSALRTERVFRALKATSVISGLVIVCALLRSVKK	249
Db	188	DPNNWLDTSVVMAYTEFV--SLGNVSALRTERVRLURALKTISVIPGLKTIYCALIQSVK	246
QY	250	LVDVWLTLFCLISIFALVGOQLFMGLNOKIKIHCNPGNPASNKDCFKEKDS-----	302
Db	247	LSDWMILTVECLSVFALIGLQLFMGLNRNKLQW-----PPSD-SAPETNTTSFNGTMD	300
QY	303	-----EDFTMCGTWLGRPCPNCGSTCKTTLNPD	331
Db	301	SNCTFVNVTMTSTFNWKDYIGDSSHFYVLDGQKDPDLCGNSDAGQCPEGYTCVAGRNP	360
QY	332	NNYTKEDNFCWSPFLAMFRVMTQDSWERYRQILRTSGIYFVFVWIFLGSFYLLNLT	391
Db	361	YGYTSEDTSWAPLSLFRMTQDYENLXQLTLRANGKTYMIFVFLVFLGSFYVLNLI	420
QY	392	AVVTMAYEQNRNVAETAKEKMTQEAQOOLLREBEKALVAM-----GIDR	437
Db	421	AVVAMAYEQNATLEAEQKEAEQOMLEQLKKQOEQAQVAAASARDFSGTIGGLGE	480
QY	438	SSLNSLQASSFSPPKKKFFGS---FKRSFFMRGSKTAQASA---SDSEDDASKNPOLLE	491
Db	481	LLSESSAEKLSKSAAKENRRKKRQREHLEGNKKGERDSFPKSESDSVKRSFLFS	540
QY	492	QT--KRUS-----QNLVVDLF-----DEH-----	508
Db	541	MDGNRLTSDKKFCSPHQSLLSINGSLFSPRRNSKTSIFSFGRAKDVGSENFADDEHST	600
QY	509	-----VDPLHROARSANV	521
Db	601	FEDSESRDLSFVPHRHGERRNSNGTTTETEVKRRRLSSYQISMEMLDESSCRORAVSIA	660
QY	522	SILTITIQOEKQPEPCFCGKNLASKYLWDPSCQWLCKIKKVLRTIMTDPFTELAITIC	581
Db	661	SILTMTWEELESROKPCPCWYRFANVFLIWDCCDAWLKXHLVNLVIMDFEVDLAIITC	720
QY	582	IIINTVFLAVEHHNMDNLKTILKIGNVFTGTGIFTAEMCLKIIALDPHYFHRGHWPDFS	641
Db	721	IVLNTLFMAEHYPMTQEFSVTLVGNLVFTGTFTAEMVLKTIAMDPYYIEQEGNIPDG	780
QY	642	IVALLSLADLVLYNTLSDNNRSLASLRLVRVFKLAKSMTPLNTLTKIIGHSVGALGNLTV	701
Db	781	IIVSLSLMELGLSNV--EGLSVLRSEFLRLVRVFKLAKSMTPLNMLKIIIGNSVGALGNLT	838
QY	702	VLTIVVFIYSVGMRLFGTKFNK--TAYATQERPRRRHMDNFYHSFLVYFRLIGCEWTEN	760
Db	839	VLAIIIVFIYAVGMQLGFSYKECVCKINDDCTLPRWHMDDFFHSHSLIVFRVLGCEWIE	898
QY	761	MWCMODMDGSLPCIIVFVLVIGKLVNLNFIALLNFSNNEEKOSLGEGERTKYKVQ	820
Db	899	MWDCM--EVAGQTMCLLIVFVLVWVGNLVNLNFIALLSSFSDDL--AATDDDNEMNNLQ	956
QY	821	LALDRFRRAFSPMLHALQSFCKCKRRKNKSPKPKETTESFAGENKDSLTPDARPKWEYDT	880
Db	957	IAYGRMQKGIYVKNMKRECFCQAFERK--PKVIEIHG-----NKIDS	998
QY	881	DMALITYGQAGAPLAPLAEVEDDVEYCGEGGALPTSOHSAGVOAGD-----	925
Db	999	CMSNNTG-----IETSKELNLRDNGT-----TSGVGTSSSVBEKYVIDENDYMSF	1044

Qy	Db	Transmem	1626	1647	S4 OF REPEAT IV.
FT	FT	TRANSMEM	1663	1685	S5 OF REPEAT IV.
FT	FT	TRANSMEM	1752	1776	S6 OF REPEAT IV.
FT	FT	DOMAIN	1905	1934	IO.
FT	FT	CARBOHYD	212	212	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	285	285	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	291	291	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	297	297	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	303	303	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	308	308	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	340	340	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	604	604	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	624	624	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	883	883	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	1055	1055	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	1072	1072	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	1136	1136	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	1368	1368	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	1382	1382	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT	CARBOHYD	1393	1393	N-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE	2005 AA; 227872 MW; 861BE58D79F8324 CRC64;			
Query Match					
Best Local Similarity 48.9%; Score 4484.5; DB 1; Length 2005;					
Matches 950; Conservative 278; Mismatches 448; Indels 301; Gaps					
Qy	Db	11	PDERNRPFSDSLAAIKKRIATQK-----ERKSKDKAAAEPOPPOLDLKAQRKLPK	64	
Qy	Db	9	PGDPSRFFPRSLAAIEQRIAEKAKRPQERKDEDD-----ENGPKNSDLEAKRSLDPF	64	
Qy	Db	65	LYGDIPELVTKPLEDDPYVKDHKTFTVLNKKRTTYRFSAKRALFILGPNPLRSLMTR	124	
Qy	Db	65	IYGDIPPEVSEPLEDDPYVINKKTFVLNKGKALSRESATSALYILTFPNPIRKLAIK	124	
Qy	Db	125	ISWHSVFSMFICTVYIINCMFAMNSWERSGFDNDIPYVFIGIYIILEAVIKILARGFVDE	184	
Qy	Db	125	ILVHSLFNVLIMCTILTNCFVMTSMNPDPWTKNV-EYTFGTGYTFESLIKILARGFCLEBD	183	
Qy	Db	185	FSELROPWNWLDFTIVIGTALATCFPGSQVNLSALRTFRVFRALKALTSVIGLKIVGALL	244	
Qy	Db	184	FTLELRPNWMLDFTVITFAVTEFV-NLGVNSALRTFRVLRALKLTISVIPGLKTIIVGALI	242	
Qy	Db	245	RSVKKLVDVWVLFLFCISIFALVGQOLFIMGILNKKCIKHNCGPNASN-----	292	
Qy	Db	243	QSVKKLSDVMLVFLVSLVPALIGLQFLPGLNLRNKLQW-----PDPNSTFEINITSPFN	297	
Qy	Db	293	-----KDCFEKEKDSDEFTMCGTWMVLSGRPCPNGSTCDKTT	327	
Qy	Db	298	NSLDWNGTAFNRVTNVMFNWDEYIEDKSHFYLEGQNDALLCGNSSDAGOCPEGYICVKAQ	357	
Qy	Db	328	LNPDNNYTKFDNCGWFLAMFRVMTODSERLYRQILRTSGIVFYVFFVVVFLGSLFYLL	387	
Qy	Db	358	RNPNGYTSDETFSWAFLSFLRMLTQDFWENLYQLTLRAAGKTYMIFFLVLVFLGSLFYLI	417	
Qy	Db	388	NLTAVVTMAIEQNRRVAETAETAEKEMFOE-AQOLLREKEKALVAN-----	433	
Qy	Db	418	NLILAVVAMAYEQNQATLBEAQEKAEAFQOMLEQLKKQOBEAQAAAAAASERDFSCA	477	
Qy	Db	434	-GIDRSSLSLQASFPKRRKFFGSKTRK-----	462	
Qy	Db	478	GGIGVFSESSVASKLSSKSEKELKNRRKKKKQEQAEKEEKEDAVRKSASEDSIRKKGF	537	
Qy	Db	463	SFMWRSKTAQ-----ASASISDEDD-----	482	
Qy	Db	538	QFSLGSRRLTYEKRFSPHQSLLSIRGSLFSPRRNSRASLFNPKGRVKYKIGENDFADDE	597	
Qy	Db	483	-----ASKNPOLLEQTKRLSONLPV-----	502	
Qy	Db	598	HSTFEDNDSRDLFLFVPHRIGERRPNSVQASRASRGITPLMNGKMHSAVDCNGVSVLV	657	
Qy	Db	503	-----DLFDE-----HV-----DPLHQRALSAVSILITITIQ	529	

QY 1105 FLIVVVSVLSL-----MNPSPKSFRTLRALRPLRALSGFEGMKVVVVYALISAIPAIL 1157
DB 1289 FLIVDVSLVSTANALGYSELGAIKSLRTRALRPLRALSGFEGMRVVVVNALLGAIPSM 1348
QY 1158 NVLLVCLLFWLFCILGVNLSGKGRGRCINGTDINWYLDFTVEVPRNSOC-----NISVYS 1212
DB 1349 NVLLVCLLFWLFLFSMGVNLFAKGYHCVTNTTGTDF-EITEVNNHSDCLLIERNETAR 1407
QY 1213 WKVPQVNDVGNVAYLALLQVATYKGLWEIMNAAVDSREKDEQDFEALNAYLVFVFI 1272
DB 1408 WKNVKVNFDNFGVLSLQVATFKGMDIMYAAVDSRNVELQPKYESLWYLVFVFI 1467
QY 1273 IFGSFNTLNLFGVLIIDNFNOOKKLGODIFMTEEQKYYNAMKKGKPKQPIRPL 1332
DB 1468 IFGSFNTLNLFGVLIIDNFNOOKKFGODIFMTEEQKYYNAMKKGKPKQPIRPRG 1527
QY 1333 NKQAFVFDLVSQFVDFVILGLVNLIMMAESADOPKDKVTFDILNFAVVFIE 1392
DB 1528 NKFGQWVDFVTRQVDFDISIMILICLNMVMTMVEDDQSDYVTSLSRLNLFVILFTGE 1587
QY 1393 CLIKVFLRQHYFTNGWNLFCVGVVYVLSIISTLVNRL-EDSDISPPPTLFRVRLARIGR 1451
DB 1588 CVLKILSRHYFTTGNIFPVVVVLSVGMFAELKEKTFVS--PTLFRVRLARIGR 1645
QY 1452 IRLVRAARGINTLFLALMMSLPNLFNIGLLFLVMFYAIFGMSWFSKVKKSGDIDIF 1511
DB 1646 IRLIKGAKGINTLFLALMMSLPALFNIGLLFLVMFYAIFGMSNFAVYKRVGIDDMF 1705
QY 1512 NFEPFTGSMCLFQITTSAGWDTLNPMLEAK-EHCN-----SSSDSCQOQPOIAVY 1563
DB 1706 NFETEGNSMICLFQITTSAGWDGLLAPILNSKPPDCDPKNVPGSVKGDGPNVSGVFF 1765
QY 1564 FVSYIIIFLIVNMYIAVILENFTATESEDDPLGEDDFETFEVWEKEDPEASOFTQY 1623
DB 1766 FVSYIIIFLIVNMYIAVILENFTATESEDDPEASEPLUSEDDEFYEVWEKEDPDATQFMEF 1825
QY 1624 SALSDFADALPEPLRAKPNKQFQLVMDLPVMVMDRLCHMDVLFATFTRVLGDSGLDTM 1683
DB 1826 EKLMSQFAALEPPLPQNPQLQILAMDLPVYSGDRIHCLDILFATFTRVLGSEGDAL 1885
QY 1684 KTMEEKKEWNEANPKLEPIVTTTKRKEEBOGGAIVRAYRKHKMEK 1730
DB 1886 RIOMEEREPFASNPVSKVSYQPTITTLKRKQEEVSAVIRYRRHLK 1932
RESULT 9
CIN4_RAT STANDARD: PRT: 1840 AA.
ID CIN4_RAT
AC P15390;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE ALPHA-SUBUNIT (MU-1).
GN SCN4A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148778; PubMed=2559760;
RA Trimmer J.S., Cooperman S.S., Tomiko S.A., Zhou J., Crean S.M.,
RA Boyle M.B., Kallen R.G., Sheng Z., Barchi R.L., Sigworth F.J.,
RA Goodman R.H., Agnew W.S., Mandel G.
RT "Primary structure and functional expression of a mammalian skeletal
muscle sodium channel.";
RL Neuron 3:33-49(1989).
CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT. THIS SODIUM CHANNEL MAY BE PRESENT IN BOTH DENERVATED
CC

AND INNERVATED SKELETAL MUSCLE.
-!- SUBUNIT: MUSCLE SODIUM CHANNELS CONTAIN AN ALPHA SUBUNIT AND A
SMALLER BETA SUBUNIT.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
-!- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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or send an email to license@isb-sib.ch).

EMBL; M26643; AAA41682.1; -
PIR; JN0007; CHRTM1.
InterPro: IPR002111; Cat_channel_TrpL.
InterPro: IPR000636; Cation_chan_non_lig.
InterPro: IPR001682; Channel_pore_Ca_Na.
InterPro: IPR000048; IQ.
InterPro: IPR001696; Na_channel.
Pfam: PF00520; ion_trans; 4.
Pfam: PF00612; IQ; 1.
PRINTS; PR00170; NACHANNEL.
SMART; SM00015; IQ; 1.
PROSITE; PS50096; IQ; 1.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Glycoprotein; Repeat; Multigene family; Phosphorylation.
FT TRANSMEM 130 152 S1 OF REPEAT I.
FT TRANSMEM 156 179 S2 OF REPEAT I.
FT TRANSMEM 192 212 S3 OF REPEAT I.
FT TRANSMEM 214 233 S4 OF REPEAT I.
FT TRANSMEM 252 274 S5 OF REPEAT I.
FT TRANSMEM 417 444 S6 OF REPEAT I.
FT TRANSMEM 571 593 S1 OF REPEAT II.
FT TRANSMEM 663 685 S2 OF REPEAT II.
FT TRANSMEM 696 721 S3 OF REPEAT II.
FT TRANSMEM 722 737 S4 OF REPEAT II.
FT TRANSMEM 756 778 S5 OF REPEAT II.
FT TRANSMEM 832 859 S6 OF REPEAT II.
FT TRANSMEM 1084 1105 S1 OF REPEAT III.
FT TRANSMEM 1117 1140 S2 OF REPEAT III.
FT TRANSMEM 1149 1168 S3 OF REPEAT III.
FT TRANSMEM 1176 1195 S4 OF REPEAT III.
FT TRANSMEM 1215 1236 S5 OF REPEAT III.
FT TRANSMEM 1324 1351 S6 OF REPEAT III.
FT TRANSMEM 1405 1427 S1 OF REPEAT IV.
FT TRANSMEM 1437 1460 S2 OF REPEAT IV.
FT TRANSMEM 1468 1487 S3 OF REPEAT IV.
FT TRANSMEM 1502 1522 S4 OF REPEAT IV.
FT TRANSMEM 1535 1556 S5 OF REPEAT IV.
FT TRANSMEM 1627 1653 S6 OF REPEAT IV.
FT DOMAIN 1720 1749 IQ.
FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 502 502 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 954 954 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MOD_RES 56 56 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 251 251 (POTENTIAL).
FT MOD_RES 251 251 PHOSPHORYLATION (BY CAPK)

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92134303; PubMed=1310396;
RA Wang J., Rojas C.V., Zhou J., Schwartz L.S., Nicholas H.,
RA Hofmann E.P.;
RT "Sequence and genomic structure of the human adult skeletal muscle
RT sodium channel alpha subunit gene on 17q.";
RL Biochem. Biophys. Res. Commun. 182:794-801(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93338444; PubMed=1339144;
RA McClatchey A.I., Lin C.S., Wang J., Hoffman E.P., Rojas C.V.,
RA Gusella J.F.;
RT "The genomic structure of the human skeletal muscle sodium channel
RT gene.";
RL Hum. Mol. Genet. 1:521-521(1992).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=92246457; PubMed=1315496;
RA George A.L. Jr., Komisarof J., Kallen R.G., Barchi R.L.;
RT "Primary structure of the adult human skeletal muscle voltage-
RT dependent sodium channel.";
RL Ann. Neurol. 31:131-137(1992).
[4]
RP VARIANT MET-704.
RX MEDLINE=92069747; PubMed=1659948;
RA Ptacek L.J., George A.L. Jr., Griggs R.C., Tawil R., Kallen R.G.,
RA Barchi R.L., Robertson M., Leppert M.F.;
RT "Identification of a mutation in the gene causing hyperkalemic
RT periodic paralysis.";
RL Cell 67:1021-1027(1991).
[5]
RP VARIANT PMC VAL-1592.
RX MEDLINE=92065978; PubMed=1659668;
RA Rojas C.V., Wang J., Schwartz L.S., Hoffman E.P., Powell B.R.,
RA Brown R.H. Jr.;
RT "A Met-to-Val mutation in the skeletal muscle Na+ channel alpha-
RT subunit in hyperkalemic periodic paralysis.";
RL Nature 354:387-389(1991).
[6]
RP VARIANTS PMC VAL-1306 AND MET-1313.
RX MEDLINE=92154689; PubMed=1310898;
RA McClatchey A.I., van den Berg P., Pericak-Vance M.A., Raskind W.,
RA Verellen C., McKenna-Yasek D., Rao K., Haines J.L., Bird T.,
RA Brown R.H. Jr., Gusella J.F.;
RT "Temperature-sensitive mutations in the III-IV cytoplasmic loop
RT region of the skeletal muscle sodium channel gene in paramyotonia
RT congenita.";
RL Cell 68:769-774(1992).
[7]
RP VARIANTS PMC PHE-804 AND THR-1156.
RX MEDLINE=93265141; PubMed=1338909;
RA McClatchey A.I., McKenna-Yasek D., Cros D., Worthen H.G., Kuncel R.W.,
RA Desilva S.M., Cornblath D.R., Gusella J.F., Brown R.H. Jr.;
RT "Novel mutations in families with unusual and variable disorders of
RT the skeletal muscle sodium channel.";
RL Nat. Genet. 2:148-152(1992).
[8]
RP VARIANTS PMC CYS-1448 AND HIS-1448.
RX MEDLINE=92265302; PubMed=1316765;
RA Ptacek L.J., George A.L. Jr., Barchi R.L., Griggs R.C., Riggs J.E.,
RA Robertson M., Leppert M.F.;
RT "Mutations in an S4 segment of the adult skeletal muscle sodium
RT channel cause paramyotonia congenita.";
RL Neuron 8:891-897(1992).
[9]
RP VARIANT PMC ARG-1433.
RX MEDLINE=93270429; PubMed=8388676;
Ptacek L.J., Gouw L., Kwiecinski H., McManis P., Mendell J.R.,
Barnoh R.J., George A.L. Jr., Barchi R.L., Robertson M., Leppert M.F.;
"Sodium channel mutations in paramyotonia congenita and hyperkalemic
periodic paralysis.";
Ann. Neurol. 33:300-307(1993).
[10]
RP VARIANTS PMC ALA-1306; GLU-1306 AND VAL-1306.
RX MEDLINE=94141728; PubMed=8308722;
RA Lerche H., Heine R., Pika U., George A.L. Jr., Mitrovic N.,
RA Brottatzki M., Welss T., Rivet-Bastide M., Franke C., Lomonaco M.,
RA Ricker K., Lehmann-Horn F.;
RT "Human sodium channel myotonia: slowed channel inactivation due to
RT substitutions for a glycine within the III-IV linker.";
RL J. Physiol. (Lond) 470:13-22(1993).
[11]
RP VARIANT PMC MET-1589.
RX MEDLINE=94061027; PubMed=8242056;
RA Heine R., Pika U., Lehmann-Horn F.;
RT "A novel SCN4A mutation causing myotonia aggravated by cold and
RT potassium.";
RL Hum. Mol. Genet. 2:1349-1353(1993).
[12]
RP VARIANT PMC ILE-1293.
RX MEDLINE=96154961; PubMed=8580427;
RA Koch M.C., Baumbach K., George A.L., Ricker K.;
RT "Paramyotonia congenita without paralysis on exposure to cold: a novel
RT mutation in the SCN4A gene (Val1293Ile).";
RL Neuroreport 6:2001-2004(1995).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE. THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT. THIS SODIUM CHANNEL MAY BE PRESENT IN BOTH DENERVATED
AND INNERVATED SKELETAL MUSCLE.
-1- SUBUNIT: MUSCLE SODIUM CHANNELS CONTAIN AN ALPHA SUBUNIT AND A
SMALLER BETA SUBUNIT.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
SEGMENT (S4).. SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
-1- DISEASE: DEFECTS IN SCN4A ARE THE CAUSE OF BOTH HYPERKALEMIC
PERIODIC PARALYSIS (HYPP) AND PARAMYOTONIA CONGENITA (PMC) WHICH
ARE NOW BOTH KNOWN AS SODIUM CHANNEL DISEASE. CHARACTERIZED BY
MUSCLE STIFFNESS DUE TO MEMBRANE HYPEREXCITABILITY.
-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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EMBL; L01983; AAA75557.1; ALT_SEQ.
EMBL; L01962; AAA75557.1; JOINED.
EMBL; L01963; AAA75557.1; JOINED.
EMBL; L01964; AAA75557.1; JOINED.
EMBL; L01965; AAA75557.1; JOINED.
EMBL; L01966; AAA75557.1; JOINED.
EMBL; L01967; AAA75557.1; JOINED.
EMBL; L01968; AAA75557.1; JOINED.
EMBL; L01969; AAA75557.1; JOINED.
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EMBL; L01975; AAA75557.1; JOINED.

DR EMBL; L01976; AAA75557.1; JOINED.
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DR EMBL; L01978; AAA75557.1; JOINED.
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DR EMBL; L04235; AAB59624.1; JOINED.
DR EMBL; M81758; AAB60554.1; JOINED.
DR EMBL; S82622; AAB21450.2; JOINED.
DR PIR; A42099; AS2099.
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DR MIM; 170500; -.
DR MIM; 168300; -.
DR MIM; 168350; -.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; Catlon_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS00096; IQ; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Repeat; Multigene family; Phosphorylation;
Query Match 47.4%; Score 4347.5; DB 1; Length 1836;
Best Local Similarity 49.2%; Pred. No. 7.8e-268;
Matches 906; Conservative 272; Mismatches 416; Indels 249; Gaps 35;
Qy 17 RPTFSDSLAAIKKRIATQKERR--KSKDKAAAEQPRQLDLKASRKLPLKLYGDIPPELV 74
Dy 18 RPTFRESLAAEQR-AVEEAEARLQNKQMEIEEPKPRSDLEAGKNLPMLYGPDPPEVI 76
Qy 75 TKPLEDDPYKDHKTFLVNLKRTIYRFSAKRALFILGPNPLRSMLIRSVHSVFSMF 134
Dy 77 GIPLEDDPYYSNKTFTVLNKAIFAESATPALYLLSPFSVVRGAIKVLIHALFSMF 136
Qy 135 ICTVTINCMPMANSERSFNDIPEYVFIGIYILEAVIKILARGFIVDFESFLRDPNNW 194
Dy 137 IMITILTNCVPMWSDPPWPKNV-EYFTGIYTFESLIKILARGFCVDDFTFLRDPNNW 195
Qy 195 LDFIVIGTAICPPGSOVNLISALRTFVFRALKKAISVISGLKVIYVALLRSVKLLVDVM 254
Dy 196 LDFSVIMMAYLTERV-DLGNISALRTFVRLALTKITVIGPKTIVGALIQSVKLLSDVM 254
Qy 255 VTLFCLISFALVGOQLFMGLINOKIKHNCGPNPASN----- 292
Dy 255 ILTVCLSVFALVQLFMGLNLRQKVR--WPPPPNDNTWTWYNDTWYGNEM 311
Qy 293 -----KDCFEXE-----KDSEDFIMCGTWLGRPCPN 319

312 WYGNDSVYANDTWNASHASWATNDFDMDAYISDEGNFYFLEGSNDALCNGSSDAGHCPO 371
Qy 320 GSTCDKTTLNPDNNYTKFDNEGWSFLAMFRVMTQDSWRLRQLRLTSGIYFVFFVVI 379
Dy 372 GYECIKTGRNPNYGYTSYDTFSWAFALFLRLMTQDYNLQTLRLAAGKYMIFVVI 431
Qy 380 FLGSFYLLNLFLAVVYMAEYEQNRNVAATEAKEMKFOEAQOOLREKEALVAMGIDRSS 439
Dy 432 FLGSFYLLNLFLAVVYMAEYEQNRNVAATEAKEMKFOEAQOOLREKEALVAMGIDRSS 482
Qy 440 LNSLQASSFSKPKKFFGSKTRKSEFFMRGSKTAQA---SASDEDDASNPOLLQOTKRL 496
Dy 483 -----EKAQAALAEAGEADGDPHAKGDCNGSLDTSQG 515
Qy 497 SONLPVOLFDEHVDPLHRQRALSASVILTIITQEOKEQEPFCPCGKNLASKYLWDCSP 556
Dy 516 EKGAP-----RQSGSGSGISDAMEELEEAHOKCPWYKCAKHYLIWNC 562
Qy 557 QWLCIKKVLRTIMTDPFTELAIITIIINTVFLAVEHHMDDNKLTKILKIGNWFTGIFI 616
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Qy 617 AEMCLKIITLDPYHYFRHGNVFDISIVALLSLADV-LYNTLSNRSFLASLRVLRVKL 675
Dy 623 AEMVLKLIAMDPEYFQOGWNIIDSIIYVLSLVELGLANV---OGLSVLSRFLRLVRVKL 679
Qy 676 AKSWPTLNLTKIIGHSGVAGLNLTVTVIVFISVVMRLFGTKENK-TAYATOERPR 734
Dy 680 AKSWPTLNLTKIIGHSGVAGLNLTVTVIVFISVVMRLFGTKENK-TAYATOERPR 739
Qy 735 RRWHMDFYHSFLVVRILCGEWIENMGCMQMDGSPICIIIVFLIMVIGLVVNLFI 794
Dy 740 PRWHMDFYHSFLVVRILCGEWIENMGCMQMDGSPICIIIVFLIMVIGLVVNLFI 798
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Dy 799 ALLNSPSNE-----EKDGSLEGETRKTQVQLALDRPRASF-----MLHALQSICC 846
Qy 843 KKRKRNKPKPKETTESF-----AGENKDSILPDAR--PWKE--YDTDMALYTGQA 889
Dy 847 -----KILSPRDIIMLSLGEADGAGEGGETAPEDKKEPPEDELLKDNHILNMG 900
Qy 890 GAP-----LAPLAEVDDVEYCGEGGALPTSQHSAGVQAGLPPET 930
Dy 901 DGPPSSLELDHLNFINNPLYTIQVPIASESDLE-----MPTEE-----ET 941
Qy 931 KOLTSPODQGVEMEVSEEDLHLSIOSPRKSDAVSMISECSTIDLNIFRNLOKTV--S 988
Dy 942 DTFSEPED-----SKKPPQPLYDGNS--SVCSTADYKPPPEDEPPEQABEN 984
Qy 989 PK-KOPDRCFKGLSCHFLCHKTOKRSPWLVNWNIRKTCYQIVKHSFESFIFVILLS 1047
Dy 985 PEGSOPBECFTEACQVRWPCLYVDISQGRKKWTLRRACFKIVEHNNFTFIVFMILLS 1044
Qy 1048 SGALIFEDVNLPSRPQVEKLLRCDNIFTIFLLEMLKLVAFGRFRFTSAWCHDELFI 1107
Dy 1045 SGALAFEDIYIEQRRVIRITILEYADKVTYIFIMELKLVAFGRFRFTSAWCHDELFI 1104
Qy 1108 VVSVLSLM-----NLPSLKSFTLRALRALSOFEGKVVVYVYALISAIPAILNV 1160
Dy 1105 VDVSTIISLVANMLGYSELGPIKSLRTRALRALSOFEGKVVVYVYVYVYVYVYVYVYVY 1164
Qy 1161 LVCLIFLWFLCIVLGNLFSKFGKRCINGCTDINMYLDFTVEPNRSOC-----NISNYSKVP 1216
Dy 1165 LVCLIFLWFLCIVLGNLFSKFGKRCINGCTDINMYLDFTVEPNRSOC-----NISNYSKVP 1223
Qy 1217 QVNFQNVGNALVALQVATYKGLWLEIMNAADVSRKQDPQDFEALYLYFVVFVIFGS 1276
Dy 1224 KVNVDNGLYLVLLOVATFKGWDIMYVAVDSRKEQPOQYEVNLYWYLVFVIFGS 1283
Qy 1277 FFTLNLFTGVITDNFNQOQKGLGGQDIFMTEEQKYNAKMKLGTKPKQKPIPRPNKCQ 1336
Dy 1277 FFTLNLFTGVITDNFNQOQKGLGGQDIFMTEEQKYNAKMKLGTKPKQKPIPRPNKCQ 1336

Db 1284 FFTLNLFGLVINDFNQKKLGGKIDFMTBEQKYYNAMKKLGGKPKQPIPRPNQKIQ 1343
Qy 1337 AFVDELVSQVDFVILGLVNLIMMAESADQPKVKTFDIL---NIAFVVIFTEC 1393
Db 1344 GWYDLVTKQAFDITIMILCLNMVMTVETDDQS---QLKVDILYNINMIFIIIFTGEC 1400
Qy 1394 LIKVPALRQHYFTNGWNLFCDCVVVLSITISLVSRLESDISFPPTLFRVRLARIGRL 1453
Db 1401 VLKMLALQXYFTVGNWIFDFVVLISVIGLALSLQK-YFVSTPLFRVRLARIGRLV 1459
Qy 1454 RLVARAARGIRTLFALMMSLPLFNIGLGLFLVMFIYAIFGMSFVKYKGGSGDDIRNF 1513
Db 1460 RLIRGAKGIRTLFALMMSLPLFNIGLGLFLVMFIYIFGMSFVKYKGGSGDDIRNF 1519
Qy 1514 EFTGSMCLCQITTSAGWDILLNPMLEA-----KEHCNSSQSDSCQPOQTAIVYFV 1565
Db 1520 EFTGSMCLCQITTSAGWDILLNPMLEA-----KEHCNSSQSDSCQPOQTAIVYFV 1579
Qy 1566 SYIIISFLVVMYIAVILENFNTATESEDPGLGDDFEIYEVWEKFDPEASOFIOYSA 1625
Db 1580 SYIIISFLVVMYIAVILENFNTATESEDPGLGDDFEIYEVWEKFDPEASOFIOYSA 1639
Qy 1626 LSFADALPELRLVAKPNKQFVLMDLPMVMDGRHLCMDVLFATFTRVLGDSGLDTMKT 1685
Db 1640 LSFADALPELRLVAKPNKQFVLMDLPMVMDGRHLCMDVLFATFTRVLGDSGLDTMKT 1699
Qy 1686 MNEKFEANPEKPKLYEPIVITTRKKEEQAQVAYRKH 1728
Db 1700 MNEKFEANPEKPKLYEPIVITTRKKEEQAQVAYRKH 1742

RESULT 11
CINA_ELEEL STANDARD; PRT; 1820 AA.
ID CINA_ELEEL AC P02719;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE SODIUM CHANNEL PROTEIN (NA+ CHANNEL).
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Gymnotiformes; Electrophoridae; Electrophorus.
OX NCBI_TaxID=8005;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85061498; PubMed=6209577;
RA Noda M., Shimizu S., Tanabe T., Takai T., Kayano T., Ikeda T.,
RA Takahashi H., Nakayama H., Kanaoka Y., Minamino N., Kangawa K.,
RA Matsuo H., Raftery M.A., Hirose T., Inayama S., Hayashida H.,
RA Miyata T., Numa S.;
RT "Primary structure of Electrophorus electricus sodium channel deduced
RT from cDNA sequence.";
RL Nature 312:121-127(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87311395; PubMed=2442385;
RA Noda M., Numa S.;
RT "Structure and function of sodium channel.";
RJ J. Recept. Res. 7:467-497(1987).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
CC PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
CC WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
CC HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
CC SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- MISCELLANEOUS: AVAILABLE DATA SUGGEST THAT ACTIVATION AND

INACTIVATION GATES ARE LOCATED NEAR THE CYTOPLASMIC SURFACE OF THE
MEMBRANE. IT IS HYPOTHESIZED THAT RESIDUES 802-806, 847-857,
894-910, AND 942-955 MIGHT, IN CONJUNCTION WITH THE POSITIVELY
CHARGED RESIDUES OF S4, ACT AS A VOLTAGE SENSOR INVOLVED WITH THE
ACTIVATION GATE.
CC -1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
CC
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CC
CC EMBL; X01119; CAA25587.1; -;
CC EMBL; M22252; AAA79960.1; -;
CC PIR; A03178; CHEE.
CC InterPro; IPR002111; Cat_Channel_TrpL.
CC InterPro; IPR000636; Cation_chan_non_lig.
CC InterPro; IPR001682; Channel_pore_Ca_Na.
CC InterPro; IPR001696; Na_channel.
CC Pfam; PF00520; ion_trans; 4.
CC PRINTS; PR00170; NACHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Repeat.
CC FT REPEAT 111 419 I.
CC FT REPEAT 555 807 II.
CC FT REPEAT 989 1281 III.
CC FT REPEAT 1311 1587 IV.
CC FT TRANSMEM 118 138 S1 OF REPEAT I.
CC FT TRANSMEM 150 171 S2 OF REPEAT I.
CC FT TRANSMEM 177 197 S3 OF REPEAT I.
CC FT TRANSMEM 204 224 S4 OF REPEAT I.
CC FT TRANSMEM 244 264 S5 OF REPEAT I.
CC FT DOMAIN 285 342 NON-HOMOLOGOUS REGION OF REPEAT I.
CC FT TRANSMEM 379 402 S6 OF REPEAT I.
CC FT TRANSMEM 558 578 S1 OF REPEAT II.
CC FT TRANSMEM 600 620 S2 OF REPEAT II.
CC FT TRANSMEM 626 643 S3 OF REPEAT II.
CC FT TRANSMEM 651 671 S4 OF REPEAT II.
CC FT TRANSMEM 691 711 S5 OF REPEAT II.
CC FT TRANSMEM 767 790 S6 OF REPEAT II.
CC FT TRANSMEM 1005 1025 S1 OF REPEAT III.
CC FT TRANSMEM 1038 1058 S2 OF REPEAT III.
CC FT TRANSMEM 1066 1086 S3 OF REPEAT III.
CC FT TRANSMEM 1092 1112 S4 OF REPEAT III.
CC FT TRANSMEM 1132 1152 S5 OF REPEAT III.
CC FT DOMAIN 1172 1194 NON-HOMOLOGOUS REGION OF REPEAT III.
CC FT TRANSMEM 1244 1264 S6 OF REPEAT III.
CC FT TRANSMEM 1321 1341 S1 OF REPEAT IV.
CC FT TRANSMEM 1353 1376 S2 OF REPEAT IV.
CC FT TRANSMEM 1381 1398 S3 OF REPEAT IV.
CC FT TRANSMEM 1417 1437 S4 OF REPEAT IV.
CC FT TRANSMEM 1454 1474 S5 OF REPEAT IV.
CC FT DOMAIN 1490 1505 NON-HOMOLOGOUS REGION OF REPEAT IV.
CC FT TRANSMEM 1544 1567 S6 OF REPEAT IV.
CC FT CARBOHYD 278 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 690 690 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 797 797 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 1160 1160 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 1174 1174 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 1820 AA; 208331 MW; 1B271F626E057864 CRC64;
Query Match 43.4%; Score 3983; DB 1; Length 1820;
Best Local Similarity 46.3%; Pred. No. 1e-244;
Matches 829; Conservative 311; Mismatches 481; Indels 170; Gaps 33;
Qy 16 FRPFTSDSLAAIKKRIATQKERRKSKDKAAAEQPRPQLDKASRLKPLVGDIPPELV 75

"Two sodium-channel genes in Drosophila: implications for channel diversity.";
Proc. Natl. Acad. Sci. U.S.A. 86:2079-2082(1989).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- ALTERNATIVE PRODUCTS: AT LEAST THREE DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PARA GENE.
-1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

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EMBL: M32078; AAB59195.1; ..
PIR: A33299; A33299.
HSP: P04002; 1WFA.
FlyBase: FBgn003036; para.
InterPro: IPR002111; Cat_channel_TrpL.
InterPro: IPR000636; Cation_chan_non_lig.
InterPro: IPR001682; Channel_pore_Ca_Na.
InterPro: IPR001696; Na_channel.
Pfam: PF00520; Ion_trans; 4.
PRINTS: PR00170; NACHANNEL.
Kw: Sodium channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Repeat; Alternative splicing; Phosphorylation.
FT REPEAT 134 467 I.
FT REPEAT 799 1069 II.
FT REPEAT 1284 1591 III.
FT REPEAT 1601 1862 IV.
FT TRANSMEM 149 172 S1 OF REPEAT I.
FT TRANSMEM 181 199 S2 OF REPEAT I.
FT TRANSMEM 213 231 S3 OF REPEAT I.
FT TRANSMEM 238 257 S4 OF REPEAT I.
FT TRANSMEM 274 297 S5 OF REPEAT I.
FT TRANSMEM 406 427 S6 OF REPEAT I.
FT TRANSMEM 813 837 S1 OF REPEAT II.
FT TRANSMEM 849 873 S2 OF REPEAT II.
FT TRANSMEM 881 900 S3 OF REPEAT II.
FT TRANSMEM 907 926 S4 OF REPEAT II.
FT TRANSMEM 942 963 S5 OF REPEAT II.
FT TRANSMEM 1014 1041 S6 OF REPEAT II.
FT TRANSMEM 1297 1320 S1 OF REPEAT III.
FT TRANSMEM 1335 1359 S2 OF REPEAT III.
FT TRANSMEM 1366 1387 S3 OF REPEAT III.
FT TRANSMEM 1392 1413 S4 OF REPEAT III.
FT TRANSMEM 1433 1454 S5 OF REPEAT III.
FT TRANSMEM 1534 1560 S6 OF REPEAT III.
FT TRANSMEM 1615 1638 S1 OF REPEAT IV.
FT TRANSMEM 1650 1673 S2 OF REPEAT IV.
FT TRANSMEM 1680 1703 S3 OF REPEAT IV.
FT TRANSMEM 1714 1735 S4 OF REPEAT IV.
FT TRANSMEM 1751 1773 S5 OF REPEAT IV.
FT TRANSMEM 1836 1860 S6 OF REPEAT IV.
FT MOD_RES 553 553 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 570 570 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 682 682 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	982	982	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1055	1055	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1180	1180	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1463	1463	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1482	1482	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1862	1862	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2047	2047	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	555	575	MISSING (IN A SPLICED FORM).
FT	VARSPLIC	1099	1121	MISSING (IN A SPLICED FORM).
FT	VARIANT	189	189	Y -> C (IN ZS20.2).
FT	VARIANT	198	198	M -> V (IN ZS20.2).
FT	VARIANT	205	205	C -> R (IN ZS20.2).
FT	SEQUENCE	2131 AA;	239385 MW;	DLECE68845A90F16 CRC64;

Query Match 38.4%; Score 3524.5; DB 1; Length 2131;
Best Local Similarity 38.1%; Pred. NO. 1.6e-215;
Matches 784; Conservative 347; Mismatches 522; Indels 407; Gaps 45;

Qy	9	IFPDERN-FRPTSDSLAAIKRIAIOKERRKSKDKAAE-----	47
Db	8	ISEERSLFRPTRESLVIOEORIAAHEKQELERKRAEGEVPRYGRKKKQKEIRYDDE	67
Qy	48	-----PQRPQLDLKASRKLKLP---KLYGDIPPELVTKPLEDLDPPYKDKHKTMLNKKRT	99
Db	68	DEDEGPQDPDPLE-----QGVPIPVRLQGSFPPELASTPLEDIDPPYSNVLTFVVVYSGKD	123
Qy	100	IYRSKRALFLGPNPLRSLMIRISVHVSFMFIICTVIINCMMFMSMERSEDNDIP	159
Db	124	IFRSKAMWMLDPFNIRVAIVILVHPLFSLEFIITILVNCILMI--MPTTVEST	181
Qy	160	EYVFIGIILVAVIKILARGFIVDEFSLRDPWNWLDIVIGTATATCFPGSQV-NLSAL	218
Db	182	EVIFGTIYTFESAVKVMARGEFLCPFTYLRDANNWLDVFIYALAYVTM--GIDLGNAAL	239
Qy	219	RTFRVERALKATSVISGLKVIIVGALLRSVKLVDMVLTFLCLSFALVGOOLEGILNQ	278
Db	240	RTFRVLRALKVAIVPGIKTIVGAVIESVKNLRDVIITMFSLSVFLMGLQIIMGVLTE	299
Qy	279	KCIK-----HNCGNPASPKNKCFEKEKSEDFIMCGTWLGSRPCNG	320
Db	300	KCIKFPDLDGSGWNLTDENWDYHN-----RNSSNWYSEDEGISFPLCNISGAGOCDD	353
Qy	321	STC-DKTTLNPDNNYTKEDNGWSFLAMFRVMTQDSWELRYQILRTSGIFVFFVVI	379
Db	354	YVLCGFGPNYGYTSDSFGWAEFLSAFLMTQDFWEDLYQLVLRAGSPWHMLFFVII	413
Qy	380	FLGSFYLLNLTLAVVTMAYEEQNRVAAETEAKEMFOEAQOLL-----	423
Db	414	FLGSFYLVNLILAIVMSYDELQKAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE	473
Qy	424	-----REEKEALVAMGIDRSSLN-441	
Db	474	AAADAAAEAAALHPMAKSPYSCISYELFVGEGKGNDDNNKMKMSIRSEVESVS	533
Qy	442	-----SLQASSSPKPKKFFGSKTKRSKSPMR-GSKTAQASA	476
Db	534	IQQPAPTAAHQATKVRKVSTTSLSLPGSPFNIR---GSRSSHKYTIIRNGRGRFPG	589
Qy	477	SDSEDDASKNPOLLBOETKRLSQNLQVLDLFDHVDPL-----	512
Db	590	SD-----RKPLVLTSTYQDAQOHLDPYADDSNAVTPMSENGALIVPVYVYGLSRHSSYT	643
Qy	513	-HRQR-----ALSAVSILITITIQEQEK-----	533
Db	644	SHQSRIYSVTHGDLGGMAVGVSTMTKESKLNRNTRNQSVMGATNGCTTCLDTNHLKLDH	703
Qy	534	-----FQEPG-----	538
Db	704	RDYEIGLECTDAGKIKIHNDNPFTEPVOTQTVVDMKDVMLNDIIEQAAGRHSRSDRGV	763
Qy	539	-----FPC-----GKNLASK-----YLVWDSCQWLICKVLRITMTDPTTELA	577

Db	764	SVYTFPTDEDDGPTFKDKALEVILKIDIVFCVWDCWCWMLKQEWVSLVIFDFFVELF	823
Qy	578	ITICIINTVFLAVEHHNNDDNLKTLIKGNMVF7GPIAEWCLKIATLDPYHVRHGWN	637
Db	824	ITLCIVNTMFAMOHDDHKNKEWELVLSGNYFFTATFAIEATWKLAMSPKYFQEGWN	883
Qy	638	VFOSIVALLSADLVYNTLSDNNRFSFLASRLVRFKIAKSWPTLNTLTKIIGHSGVALG	697
Db	884	IFDFIIVALSLELGLGEGV--OGLSVLARSFLRLRVFKIAKSWPTLNTLISIMRGTMGALG	941
Qy	698	NLTWVLTVVVFISVVGMLFC7KE--NKTAYATQERPRRRBHMNDVYHFLVVFRLTLCG	755
Db	942	NLTVFJCIITFIIVAMGLOFQKNTHDHKRPPDGDLP--RWNTDFMHSMFIVFRLVLCG	999
Qy	756	EWIENMWGCMQMDGSPGLCIIVFVILMVIWIGKVLVNLNFIALLLNSFNEEKDGSLEGETR	815
Db	1000	EWIESMWDKMYGVDVS--CIPFFLATVYIGNLVNLFLALLLSNFGS---SSLSAPTA	1053
Qy	816	---KTKVQJALDRFRRAFSFMLHALQSCKKCRK-----NSPKPKE7E-----	858
Db	1054	DNDTNKIAEAFNRIGRFSKSVWRNIAD--CFKLIRKNLNTQISDQPSGERTNOISWIWSEG	1112
Qy	859	----SFAGENKDSILPDARPKEVYTDWALVTGQAGAPLAPLAEVEDDDVEYCGEGCALP	913
Db	1113	KGVCRISAEHGDNEL-----ELGHDEILADGLIKGIEQTOLEVAI-----	1160
Qy	914	TSQHSAGVQAGDLPPTTKOLTSPDD-----QGVEME	944
Db	1161	FTI7H--GDMKNKPKSKYLLNATDDDTASINSYGSHKNRFPKDESHKSAETMEGEKR	1218
Qy	945	VFSEEDLHLSIQSPRKSDAVSMLSECTIDLN--DIFRNLQKTVSPKKQPDRCPPKGLSC	1003
Db	1219	DASKEDLGL-----DEELEDEEGCEBGLDGDIIITHAHDDEIDLDEYPADCCPD5YK	1270
Qy	1004	HELCHTKDRKSPWVLWNNIRKTCYQIVKH5WFESFIIFVL7SSGALIFEDVNLPSRPQ	1063
Db	1271	KFPILAGDDSPFQWGMGLNLUK7TRELLEDYFETAVITMILMSLALDEHLHPORPI	1330
Qy	1064	VEKLLRCTDNIFTEIFLLEMLIKWFAFGFRFYFSAMCWLDFLWVYVSLSM-----	1116
Db	1331	LQDILYIMDRIFTVIFLEMLIKWALGFKVYLTNACWCLDFVIMVYSLNFINFVASLVGAG	1390
Qy	1117	NLPSLSK7FTRLRALRPLRALSQFEGKVVVVALISAPALINVL7LCLIFWLFCILGVN	1176
Db	1391	GIQAFK7MTLRALRPLRAMSOMGRVVVVALVQAIPISEFNVL7LCLIFWLFIAMGVQ	1450
Qy	1177	LFSGK7GRC--INGTDINMYLDFTEVPARSOCSIN5YKVPQYFNEDVGNVYALLLOVA	1234
Db	1451	LFAGK7FKCEDMNGTKLSHEI---IPNRNACESNYTWVNSAMNFDHVGNAYLCL7FOVA	1506
Qy	1235	TYKGWLEIMNAVDSREKDEQDFEANYLYAVLYFVVF7IFG5FTTLNLF7GVIIDFNQO	1294
Db	1507	TFKGW7QIMNDAIDSREVDKQPIRETNIYVYLYFVF7IFG5FTTLNLF7GVIIDFNQO	1566
Qy	1295	OQKL7GO--DIPWTEBQKYYNAMKLG7KKQKPIPRPLNKCQAFVFDL7VTSQVDFVIL	1353
Db	1567	KKXAGSLEMFAT7EQKYY5SANKKXGKKPLKAIPRPRWRPQAI7VEIVTDKK7FDIIM	1626
Qy	1354	GLVL7ANMI7MAESADQPKDVK7KTDILNIAFV7L7TECLIKV7FALRQHV7F7NGWLF	1413
Db	1627	LF7GL7N7MT7LDRYDASTYNAV7LDY7NAIFV7IF5SECL7K7IFAL7HY7F7EP7NWL	1686
Qy	1414	CVV7VLSI7SL7VR--LEDSDIS7F7P7TL7FRV7RLARIGRIL7RLVRAARGI7TL7FALMS	1472
Db	1687	VVV7VLS7LGLVLSDI7EKYFVS--PTL7LRV7VAKVGRV7RL7VKGAKIGI7TL7FALMS	1744
Qy	1473	LP7SLFN7GLLL7FLV7M7YI7A7FGMSWFS7KYKGS7GIDD7INF7ET7FG7MCL7QI7TTSAGW	1532
Db	1745	LPALFNICLL7FLV7M7F7AIFGM57FMHV7KES7GINDVYNEK7FTGQ5MILL7QM7STSAGW	1804
Qy	1533	DT7LLN7PML7EAK7HCN7SSOD-----SCQOP7QI7V7YFVS7YI7IIS7FLV7NNY7AVI7LENF	1587
Db	1805	DG7VLD7RAIN--EACQPP7DDN7KG7YPCN7GCSAT7G7IFL7SVI7F7LV7IN7Y7AVI7LENY	1863

[illegible]

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Db 358 OSLKEQERR--NTLTVSEADSHVDORN-----CTCCEQ-----CCGC----- 392
QY 547 SKYLWDCSPQWLCKIKKYLRTMTDPFTELATITICIIINTVFLAVEHHNMDNLKI 606
Db 393 -----CYNPLWRVQSFACIIITDSFEVFIIFIVLINTVFLAMEHGMSELKNVLKV 445
QY 607 GNWFTGFIABMCLIIIALDPHYFRHGNVDFSDIVALLSLADLYLNTLSDNRSFLAS 666
Db 446 ANYVETTVFLEAILKLAFAK-QYFKSGWNICDLVVVASLIDLGVEGL--KGVSVFRS 502
QY 667 LRLRVFKLAKSWPTLNTLIIKIHSGVAGNLNLVTLVTVFVFSVWGMRLFGTKFNKTA 726
Db 503 FRLLRVFLAQSMTTMRLLCIILNTLGLSLGYLIIILIVIVFAVTGLQLFHTYTPDK 562
QY 727 YATQERPRRRHMDNYFSLVVRFLCGEWIENWGMCMQMDGSPLCIIVFLIMWLGK 786
Db 563 FRGEVPV--RWNFDLHSMFVFRILCGEWIEPYDCMRACNG--LCFLIFIPVTVFGK 618
QY 787 LVVLNLFIALLLNFSNEKDGSLBGETRKTKVQLALDRFRRAFSLHALQSFCCCKCR 846
Db 619 TLFF-LFGLVLGAFSDTVQOEVE-----VSSFALGPES----- 653
QY 847 RKNSPKPKETTESFAGENKSDILDPARKEYDTDMALYTOGAGAPLAPLAIVEDDVEYC 906
Db 654 -----KPCSVRERGISATDDNVKDDG-----QDEVQON 681
QY 907 GEGGALPTSQHSAGVQAGDLPEK-QLTSPDDQ--GVMEVFSEEDLHLSIQSPRKS 962
Db 682 SE-----ETKIDRNNDKQSKGMILENNCNDLSLASLGS-----L 717
QY 963 DAVSMLSECSITDLNIPNLQKTVSPKQDPKCPKGLSCHFLCHKDKRKSPPVWLWN 1022
Db 718 GSIPDIMGSSVE--DDISSCOQKIQP-----CLPLFISRFKCLREFDTSHGKKNW 770
QY 1023 IRKTCYQIVKUSWFSFIIFVILLSSGALIFEDVNLPSRQVEKLLRCDTNIFFIFILE 1082
Db 771 FRQLMVCENKPYFTGLVFIIFAFISILLAFEDIYLNKPKLAIKFIIDITFCLLFFLE 830
QY 1083 MILKVAFFGRFYFTSAMCLWDLFLVIVVSLSM-----NLPKSKFRTRLRALRPLRA 1135
Db 831 MVKLVALGVFVHYHFTHTLIDFTVIIVISLAAGLGMQITAFRSLRTRLRALRPLRA 890
QY 1136 LSQEGMKVYVYALISAPILNLVLCVILFWLFCILGVNLFSKFGRCINGTDINMYL 1195
Db 891 VSRQGMKIIIVNALMSIPSIFNVLVCVFWLFAINGVOLFAKGYKVCNET--NNRI 948
QY 1196 DTEVPNRSCQNSINYSKVPQVNDVGNAYLALLQVATYKGMLEINNAVDSREKDEQ 1255
Db 949 PPTVANKIECYNKNTVWVNSVNDVNGGAFALFQVATEFGWMEIMADAVDVEVDEQ 1008
QY 1256 PDFEANLYLVVYVFIIFGFFTLNLFVIGVINDFNQOQKLGGO--DIFWTEBOKKY 1313
Db 1009 PKFEATVYVYFVFLVFIIFGFFVNLVIGVINDKFSKLYDGTYLDMLFTPTQOY 1068
QY 1314 NAMKLGTKPKPKPIPRPLNRCQAFVFDLTVSQVDFVILGLVILNMIIMMAESADQPKD 1373
Db 1069 NTLKLGTKPKPKQVTKRPNKRCQAVVYDLVMSNOPEIFITITITNMFMAFHYNQSEV 1128
QY 1374 VKKFDILNIAFVFIITTECLIKVAFALRQHYFTGWNVLFDCVVVLSIISLVSRLESD 1433
Db 1129 VTEVLATANIAFTIAYEAIKIIGLRIHYLNWVDFDLVTLVSYMDAFNDFDGDG 1188
QY 1434 ISFPTPLFRVRLARIGRILVRAARGIRTLFLALMMSLPSLNFILGLLFLVMFIYAF 1493
Db 1189 IFMNPSSLRVARMEFGRILRIKWKAGKRLILFALVLSLFAFNIGALLMLVFIYII 1248
QY 1494 GMSWFSKVGSGIDIDIFNFTFTGSMCLFQITTSAGWDTLLNPLMPEAKHCNSS----- 1549
Db 1249 GMSWFGKILSGALNDQVNFQTFGKTFLLVRLATSAGWMDILGPLLQPCNDPNYIT 1308
QY 1550 -----SQDSQCOQPIAVVYFVSIIISFLIVVNMVIAVLENFNTATSESDPLGED 1601
Db 1309 STGEKIKVVGDCGWPWIAISYMSYIIIVFVFNMYIAVLENFNOHAQEEVGITED 1368

QY 1602 DPELFYEWKEDPEASQFIQYSALSDFADALPEPLRYAKPNKFQFLVMDLPMVMDRLH 1661
Db 1369 DLDYFYGWQYDPLATOFIKHEQUSDFIQDLDPKFKKPNVNAITFDLPVIVGGHIH 1428
QY 1662 CMDVLFATFTVRLG----DSSGLDTMKTMEKEPNEAPFKKLYBPVITVTKRKEEOGA 1717
Db 1429 CLDILLALVKALGNLEETAFKRVRTQMEARFDEIFPTREKSEIRISTLQMRREMAA 1488
QY 1718 AVIORYAK 1726
Db 1489 RTLQRAWK 1497

RESULT 15

CCAM_MUSDO
ID. CCAM_MUSDO STANDARD: PRT: 1687 AA.
AC Q25452;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1).
CS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Musca.
QC NCBI_TaxID=7370;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Muscle;
PC MEDLINE=94148084; PubMed=8313972;
KA Grabner M., Bachmann A., Rosenthal F., Striessnig J., Schultz C.,
Zautz D., Glossmann H.;
RT "Insect calcium channels. Molecular cloning of an alpha 1-subunit from
housefly (Musca domestica) muscle.";
HL FEBS Lett. 339:189-194(1994).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CELL MOTILITY, CELL DIVISION AND CELL DEATH (BY SIMILARITY). MDL-
ALPHA1 ENCODES A DIHYDROPYRIDINE- AND DILTIAZEM-SENSITIVE CURRENT
IN LARVAL BODY WALL MUSCLE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE LARVAL BODY
WALL MUSCULATURE. IN ADULTS, HIGHEST EXPRESSION IN THORAX FOLLOWED
BY HEAD AND AT A LOWER EXTENT BY ABDOMEN.
CC -!- DEVELOPMENTAL STAGE: LATE EMBRYONIC.
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIE OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
FAMILY.

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or send an email to license@isb-sib.ch).

EMBL; Z31723; CAA83514.1; -;
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.

Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Calcium channel; Glycoprotein; Repeat; Multigene family;
Calcium-binding; Phosphorylation.

KW	FT	REPEAT	48	330	I.	Query Match	16.4%	Score	1508.5	DB	1	Length	1687
KW	FT	REPEAT	420	667	II.	Best Local Similarity	25.6%	Pred. No.	9.8e-88				
FT	FT	REPEAT	777	1059	III.	Matches	449	Conservative	342	Mismatches	585	Indels	377
FT	FT	REPEAT	1096	1370	IV.	Gaps	56						
FT	DOMAIN		1	61	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		62	80	S1 OF REPEAT I (POTENTIAL).								
FT	DOMAIN		81	99	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		100	117	S2 OF REPEAT I (POTENTIAL).								
FT	DOMAIN		118	130	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		131	145	S3 OF REPEAT I (POTENTIAL).								
FT	DOMAIN		146	157	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		158	176	S4 OF REPEAT I (POTENTIAL).								
FT	DOMAIN		177	196	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		197	216	S5 OF REPEAT I (POTENTIAL).								
FT	DOMAIN		217	302	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		303	327	S6 OF REPEAT I (POTENTIAL).								
FT	DOMAIN		328	434	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		435	454	S1 OF REPEAT II (POTENTIAL).								
FT	DOMAIN		455	467	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		468	487	S2 OF REPEAT II (POTENTIAL).								
FT	DOMAIN		488	496	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		497	515	S3 OF REPEAT II (POTENTIAL).								
FT	DOMAIN		516	525	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		526	544	S4 OF REPEAT II (POTENTIAL).								
FT	DOMAIN		545	563	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		564	583	S5 OF REPEAT II (POTENTIAL).								
FT	DOMAIN		584	639	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		640	664	S6 OF REPEAT II (POTENTIAL).								
FT	DOMAIN		665	785	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		786	809	S1 OF REPEAT III (POTENTIAL).								
FT	DOMAIN		810	826	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		827	846	S2 OF REPEAT III (POTENTIAL).								
FT	DOMAIN		847	854	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		855	877	S3 OF REPEAT III (POTENTIAL).								
FT	DOMAIN		878	885	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		886	900	S4 OF REPEAT III (POTENTIAL).								
FT	DOMAIN		901	921	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		922	941	S5 OF REPEAT III (POTENTIAL).								
FT	DOMAIN		942	1030	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		1031	1055	S6 OF REPEAT III (POTENTIAL).								
FT	DOMAIN		1056	1110	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		1111	1129	S1 OF REPEAT IV (POTENTIAL).								
FT	DOMAIN		1130	1143	EXTRACELLULAR (POTENTIAL).								
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FT	DOMAIN		1164	1172	CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM		1173	1191	S3 OF REPEAT IV (POTENTIAL).								
FT	DOMAIN		1192	1219	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		1220	1238	S4 OF REPEAT IV (POTENTIAL).								
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FT	TRANSMEM		1258	1277	S5 OF REPEAT IV (POTENTIAL).								
FT	DOMAIN		1278	1343	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM		1344	1362	S6 OF REPEAT IV (POTENTIAL).								
FT	DOMAIN		1363	1687	CYTOPLASMIC (POTENTIAL).								
FT	DOMAIN		564	570	POLY-LEU.								
FT	DOMAIN		1037	1043									
FT	SITE		285	285	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).								
FT	SITE		617	617	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).								
FT	SITE		1005	1005	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).								
FT	SITE		1311	1311	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).								
FT	BINDING		979	1068	TO DIHYDROPYRIDINES (BY SIMILARITY).								
FT	BINDING		1327	1389	TO DIHYDROPYRIDINES (BY SIMILARITY).								
FT	BINDING		1337	1378	TO PHENYLALKYLAMINES (BY SIMILARITY).								
FT	MOD_RES		1378	1378	PHOSPHORYLATION (BY CAPK) (POTENTIAL).								
FT	CA_BIND		1398	1409	BY SIMILARITY.								
FT	CARBOHYD		90	90	N-LINKED (GLCNAC. . .) (POTENTIAL).								
SEQ	SEQUENCE		1687	AA: 193874	MW: 628606AFAE46DDDEF	CRG64:							

Search completed: February 27, 2002, 01:39:36
Job time: 635 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2002, 01:28:56 ; Search time 114.56 Seconds
(without alignments)
2253.585 Million cell updates/sec

Title: US-09-646-224A-2

Perfect score: 9173

Sequence: 1 MEERYYPVFPDERNRPFT.....VFCNGDLSLDVAKVKVHND 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9157	99.8	1765	11 088457	088457 rattus norv
2	8153	88.9	1765	11 09R053	09R053 mus musculu
3	8085	88.1	1765	11 09JMD4	09JMD4 mus musculu
4	6714	73.2	1791	4 09UI33	09UI33 homo sapien
5	6709	73.1	1791	4 09UHE0	09UHE0 homo sapien
6	5329	58.1	1444	4 09UHM0	09UHM0 homo sapien
7	4730	51.6	2019	11 09JUV9	09JUV9 mus musculu
8	4669	50.9	1956	6 09Y5Y9	09Y5Y9 homo sapien
9	4555	49.7	1958	11 P70276	P70276 mus musculu
10	4553	49.6	1956	11 062868	062868 rattus norv
11	4553	49.6	1977	4 Q15858	Q15858 homo sapien
12	4545	49.6	1957	11 063554	063554 rattus norv
13	4541	49.5	1984	11 008562	008562 rattus norv
14	4532	49.4	1962	6 046669	046669 canis famil
15	4515	49.2	1984	6 028644	028644 oryctolagus
16	4510	49.2	2005	4 09B2D0	09B2D0 homo sapien
17	4509	49.2	2005	4 09B2C9	09B2C9 homo sapien
18	4489	48.9	1951	4 09B2B3	09B2B3 homo sapien
19	4478	48.8	1999	4 09C008	09C008 homo sapien

20	4477	48.8	2007	13 09YGN7	09YGN7 cynops pyrr
21	4470	48.7	1951	4 09C007	09C007 homo sapien
22	4453	48.5	2000	4 09C006	09C006 homo sapien
23	4396	47.9	1978	11 09WTU3	09WTU3 mus musculu
24	4394	47.9	1978	11 088420	088420 rattus norv
25	4390	47.9	1988	11 088421	088421 rattus norv
26	4381	47.8	1840	11 070611	070611 rattus norv
27	4380	47.7	1980	4 09UQD0	09UQD0 homo sapien
28	4375	47.7	1980	4 095788	095788 homo sapien
29	4368	47.6	1732	11 060858	060858 mus musculu
30	4365	47.6	1949	13 09DF53	09DF53 brachydanio
31	4359	47.5	1841	11 09ER60	09ER60 mus musculu
32	4354	47.5	1980	4 09NYX2	09NYX2 homo sapien
33	4316	47.1	1976	11 063541	063541 rattus norv
34	4171	45.5	1880	13 09IBF1	09IBF1 takifugu pa
35	4083	44.5	1834	6 028371	028371 equus cabal
36	3918	42.7	2049	5 025150	025150 halocynthia
37	3833	41.8	1717	13 090519	090519 fugu rubrip
38	3554	38.7	2105	5 025439	025439 musca domes
39	3554	38.7	2108	5 094615	094615 musca domes
40	3550	38.7	2104	5 025440	025440 musca domes
41	3546	38.7	2031	5 001306	001306 blattella g
42	3542	38.6	2031	5 001307	001307 blattella g
43	3541	38.6	2131	5 09VXF7	09VXF7 drosophila
44	3535	38.5	2118	5 024531	024531 drosophila
45	3530	38.5	2110	5 024532	024532 drosophila

ALIGNMENTS

RESULT 1

088457	ID	088457	PRELIMINARY; PRT; 1765 AA.
AC	088457;		
DT	01-NOV-1998	(TrEMBLrel. 08, Created)	
DT	01-NOV-1998	(TrEMBLrel. 08, Last sequence update)	
DT	01-JUN-2001	(TrEMBLrel. 17, Last annotation update)	
DE	VOLTAGE-GATED NA CHANNEL ALPHA SUBUNIT NAN.		
GN	SNS2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
GX	NCBI_TaxID=10116;		
FN	[1]		
FP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;		
FX	MEDLINE=98338024; PubMed=9671787;		
RA	Dib-Hajj S.D., Tyrrell L., Black J.A., Waxman S.G.;		
RT	"NaN, a novel voltage-gated Na channel, is expressed preferentially in		
RT	peripheral sensory neurons and down-regulated after axotomy.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 95:8963-8968(1998).		
FN	[2]		
FP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;		
RA	Tate S.N.;		
FL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.		
FN	[3]		
FP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;		
FX	MEDLINE=99212311; PubMed=10196578;		
RA	Tate S.N., Benn S.C., Hick C.A., John V.H.;		
RT	"Two sodium channels contribute to the TTX-R sodium current in primary		
RT	sensory neurons.";		
RL	EMBL, Neurosci. 1:653-655(1998).		
DR	EMBL, AF059030; AAC40199.1;		
DR	EMBL, AJ237852; CAB41850.1;		
DR	InterPro: IPR000636; Cation_chan_non_lig.		
DR	InterPro: IPR000734; Lipase.		
DR	InterPro: IPR001682; Channel_pore_Ca_Na.		
DR	InterPro: IPR001696; Na_channel.		
DR	InterPro: IPR002111; Cat_channel_TrpL.		
DR	Pfam: PF00520; ion_trans; 4.		

DR PRINTS: PR00170; NACHANNEL.
DR PROSITE: PS00120; LIPASE_SBR; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1765 AA; 201843 MW; AE8C67397CC60BD9 CRC64;

Query Match 99.8%; Score 9157; DB 11; Length 1765;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1761; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEERYYPVFPDERFERPFTSDSLAAIKKRIATIAOKERKSKDAAAEQPPRLDLKASR 60
DB 1 MEERYYPVFPDERFERPFTSDSLAAIEKRIATIAOKERKSKDAAAEQPPRLDLKASR 60
QY 61 KLPKLYGDIPELVKPLEDDPYKDKHTFMVFNKKTITVRSKRALFILGPNPLRS 120
DB 61 KLPKLYGDIPELVKPLEDDPYKDKHTFMVFNKKTITVRSKRALFILGPNPLRS 120
QY 121 LMIRISVHSVSMFICTIVINCMPMANSMEKSFNDIPEYVFIIGIYLEAVIKILARGF 180
DB 121 LMIRISVHSVSMFICTIVINCMPMANSMEKSFNDIPEYVFIIGIYLEAVIKILARGF 180
QY 181 IVDEFSFLRDPNNWLDVIGTAIATCPGSOVNLALRTRVFRALKAKAISVISGLKIV 240
DB 181 IVDEFSFLRDPNNWLDVIGTAIATCPGSOVNLALRTRVFRALKAKAISVISGLKIV 240
QY 241 GALLRSVKLVDMVLTFLCLISFALVGQQLFMGLNOKICKHNGCPNPASNKDCFEK 300
DB 241 GALLRSVKLVDMVLTFLCLISFALVGQQLFMGLNOKICKHNGCPNPASNKDCFEK 300
QY 301 DSEDIMCGTWLGSRPCNGSTCDKTTLNPNNTYKDFNFGWSFLAMFRVMTQDSWERLY 360
DB 301 DSEDIMCGTWLGSRPCNGSTCDKTTLNPNNTYKDFNFGWSFLAMFRVMTQDSWERLY 360
QY 361 ROLLRTSGIYFVFPVVVIFLGSFYLLNLTAVVTMAYEQNRNVAATEAKEMFQBAQ 420
DB 361 ROLLRTSGIYFVFPVVVIFLGSFYLLNLTAVVTMAYEQNRNVAATEAKEMFQBAQ 420
QY 421 QLLREKEALVAMGIDRSLNSLOASSPFRKRRKFFGSKTSPMRGSKTAQASADSE 480
DB 421 QLLREKEALVAMGIDRSLNSLOASSPFRKRRKFFGSKTSPMRGSKTAQASADSE 480
QY 481 DDAKNPOLLSQTKRLSONLPVDLDEHVDPLHQRALSAVSILITITIOEQEKFOEPCFP 540
DB 481 DDAKNPOLLSQTKRLSONLPVDLDEHVDPLHQRALSAVSILITITIOEQEKFOEPCFP 540
QY 541 CGKNLASKYLWDCSPQWLCIKKVLRTIMTDPFTELATITICIIINTVFLAVEHHNMDNL 600
DB 541 CGKNLASKYLWDCSPQWLCIKKVLRTIMTDPFTELATITICIIINTVFLAVEHHNMDNL 600
QY 601 KTLKIGNWVFTGIFIAEMCLKIITADDPYHFRHGNVFNDSIVALLSLADVLYNTLSNN 660
DB 601 KTLKIGNWVFTGIFIAEMCLKIITADDPYHFRHGNVFNDSIVALLSLADVLYNTLSNN 660
QY 661 RSFLASRLVRVKLAKSWPTLNTLIKTIHSGVAGLNLTVLTAVTFVIFSVGMRLFGT 720
DB 661 RSFLASRLVRVKLAKSWPTLNTLIKTIHSGVAGLNLTVLTAVTFVIFSVGMRLFGT 720
QY 721 KFNKTAYATQERPRRRWHDNFYHSFLVFRILCGEWIENMGCMQMDGSPLCIIVFL 780
DB 721 KFNKTAYATQERPRRRWHDNFYHSFLVFRILCGEWIENMGCMQMDGSPLCIIVFL 780
QY 781 IMWIGKLVNLFIALINSFNEKDGSEGETRKTQVQALDRFRRAFSEFMLHALQSF 840
DB 781 IMWIGKLVNLFIALINSFNEKDGSEGETRKTQVQALDRFRRAFSEFMLHALQSF 840
QY 841 CCKKRRKNSPKPKETTESFAGENKDSILPDARPKWEYDMDALYTGQAGAPLAEVE 900
DB 841 CCKKRRKNSPKPKETTESFAGENKDSILPDARPKWEYDMDALYTGQAGAPLAEVE 900
QY 901 DDVEYGGGALPTSOHSAGVOAGDLPTETKQLTSPDQGVEMEVFSEEDLHLSIQSPRK 960
DB 901 DDVEYGGGALPTSOHSAGVOAGDLPTETKQLTSPDQGVEMEVFSEEDLHLSIQSPRK 960

QY 961 KSDAVSMLSEGSTIDLNDFRNLQKTVSPKQDRCFPKGLSCHFLCHKTDRKSPWVLW 1020
DB 961 KSDAVSMLSEGSTIDLNDFRNLQKTVSPKQDRCFPKGLSCHFLCHKTDRKSPWVLW 1020
QY 1021 WNIRKTCQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRQVEKLLRCDTNIFFTL 1080
DB 1021 WNIRKTCQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRQVEKLLRCDTNIFFTL 1080
QY 1081 LEMILKLVAFGRFRYFSAWCWLDLIVVSVLSLMLNLSKSFRTLRALRPLRALSQPE 1140
DB 1081 LEMILKLVAFGRFRYFSAWCWLDLIVVSVLSLMLNLSKSFRTLRALRPLRALSQPE 1140
QY 1141 GMKVYVYALISAIPAILNVLVCLIFLVFCILGVNLSGKFGRCINGTDINMYLDFTVE 1200
DB 1141 GMKVYVYALISAIPAILNVLVCLIFLVFCILGVNLSGKFGRCINGTDINMYLDFTVE 1200
QY 1201 PNRSCNLSNYSWKVPQVNFVNGNAYLALLQVATYKGMLEIMNAVDSREKDEQDFEA 1260
DB 1201 PNRSCNLSNYSWKVPQVNFVNGNAYLALLQVATYKGMLEIMNAVDSREKDEQDFEA 1260
QY 1261 NLYAYLYFVWFIIFGSFFTLNLFIGVIIDNFNQOQKLGQDIFMTEQKKYNNAMKLG 1320
DB 1261 NLYAYLYFVWFIIFGSFFTLNLFIGVIIDNFNQOQKLGQDIFMTEQKKYNNAMKLG 1320
QY 1321 TKKPKPIPRPLNKQAFVFDLVTQVDFVILGLILVILNMIIMMAESADQPKDVKKTFDI 1380
DB 1321 TKKPKPIPRPLNKQAFVFDLVTQVDFVILGLILVILNMIIMMAESADQPKDVKKTFDI 1380
QY 1381 LNIAPVWIFTTECLIKVEALRQHYFTNGWNLFDVGVVLSIISTLVSRLESDSIFEPPTL 1440
DB 1381 LNIAPVWIFTTECLIKVEALRQHYFTNGWNLFDVGVVLSIISTLVSRLESDSIFEPPTL 1440
QY 1441 FRVYRLARIGRILRLVRAARGIRTLFLFALMMSLPSLNFILGLLFLVMIYIIFGMSWFSK 1500
DB 1441 FRVYRLARIGRILRLVRAARGIRTLFLFALMMSLPSLNFILGLLFLVMIYIIFGMSWFSK 1500
QY 1501 VKKSGGIDIDINFETFTGSMCLFOITTSAGWDTLLNPMLEAKHCNCSQSCQOQIA 1560
DB 1501 VKKSGGIDIDINFETFTGSMCLFOITTSAGWDTLLNPMLEAKHCNCSQSCQOQIA 1560
QY 1561 VYVYVSYIIISFLIYVNNYIAVILENFNTATESEDDPLGEDDFEIFYEVWEKFDPEASQF 1620
DB 1561 VYVYVSYIIISFLIYVNNYIAVILENFNTATESEDDPLGEDDFEIFYEVWEKFDPEASQF 1620
QY 1621 IOYSALSDFADALPEPLRVAKPNKQFLVMDLPVYMGDLRHCMDVLFPAFTTRVLGDSSGL 1680
DB 1621 IOYSALSDFADALPEPLRVAKPNKQFLVMDLPVYMGDLRHCMDVLFPAFTTRVLGDSSGL 1680
QY 1681 DTMTKTMEEKFMEANPFPKLYEPIVTTTKRKEEEOGAIVORAYRKHMEKVKVLRKDKRS 1740
DB 1681 DTMTKTMEEKFMEANPFPKLYEPIVTTTKRKEEEOGAIVORAYRKHMEKVKVLRKDKRS 1740
QY 1741 SSSHQVFCNGDLSLSDVAKRVHND 1765
DB 1741 SSSHQVFCNGDLSLSDVAKRVHND 1765

RESULT 2
Q9R053 PRELIMINARY; PRT; 1765 AA.
AC Q9R053;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL NAN.
CN SCN11A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=1CR;
RX MEDLINE=99375324; PubMed=10444332;
RA Dib-Hajj S.D., Tyrrell L., Escayg A., Wood P.M., Meisler M.H.,
RA Waxman S.G.;
RT "Coding sequence, genomic organization, and conserved chromosomal
localization of the mouse gene Scn1la encoding the sodium channel
NaN";
RL Genomics 59:309-318(1999).
DR EMBL; AF118044; A053403.1; .
DR MGD; MGI:1345149; Scn1la.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR002111; cat_channel_trpl.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; ion_trans.4.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1765 AA; 201425 MW; E3F99FA896DD50A1 CRC64;

Query Match 88.98; Score 8153; DB 11; Length 1765;
Best Local Similarity 88.78; Pred. No. 0;
Matches 1569; Conservative 94; Mismatches 99; Indels 6; Gaps 5;

Qy 1 MEERYYPVIFPDERNFRPFTSDSLAAIKKRIATQKERRKSKDKAAAEQPRPQLDLKASR 60
Db 1 MEERYYPVIFPDERNFRPFTSDSLAAIEKRITIQEKKKSKDKAAATEPQPRPQLDLKASR 60

Qy 61 KLPKLYGDIPELVTKPLEDDPYKHDKHTFWLNKKRTIYRFSAKRALFILGPPNPURS 120
Db 61 KLPKLYGDPVPLIAKPLEDDPYKHDKHTFWLNKKRTIYRFSAKRALFILGPPNPURS 120

Qy 121 LMRISVHSVSMFTICVINCMPMAN--SMERSFNDIDPEYFYGIVYLEAVTKILAR 178
Db 121 FMIRISVHSVSMFTICVINCMPMANNSVDSRSPSSNPEYFYGIVYLEAVTKILAR 180

Qy 179 GFIVDEFSLRDPNNWLDIVIGTAIATCFPGSQV-NLSALRTFRVFRALKAISVISGLK 237
Db 181 GFIVDEFSYLRDPNNWLDIVIGTAIAPCFGLGNKVNLLSTLRPRVLRALKAISVISGLK 240

Qy 238 VIVGALLRSVKLVDMVWVLTFLCSIFALVGOQLFMGLNOKCTKHNGCPNPASNKDCFE 297
Db 241 VIVGALLRSVKLVDMVWVLTFLCSIFALVGOQLFMGLNOKCTKHNGCPNPASNKDCFE 300

Qy 298 KEKQSEDFIMGTVLGSRPCNGSTCDKTTLPDNNYTKFDNFGSHFLAMFRVMTQDSWE 357
Db 301 KENQSEDFIMCGNLGRRCSDPGSTCKTTFNPDYNTFDSFGSHFLAMFRVMTQDSWE 360

Qy 358 RLYRQILRTSGIYFVFVVFVIFLGSFYLLNLTLAVVTMAYEEOQNRNVAATEAKEKMFQ 417
Db 361 KLYRQILRTSGIYFVFVVFVIFLGSFYLLNLTLAVVTMAYEEOQNRNVAATEAKEKMFQ 420

Qy 418 EAQQLLREKALVAMGIDRSLSLQASFSPPKRRKFFGSKTRKSFPMRGSKTAQASAS 477
Db 421 EAQQLLREKALVAMGIDRTSLNSLQASFSPPKRRKFFGSKTRKSFPMRGSKTARASAS 480

Qy 478 DSEDDASKNPOLLLEOTKRLSONLPDLDEHVDPLHRRORALSAYSILITITOEQKFOEP 537
Db 481 DSEDDASKNPOLLLEOTKRLSONLPVELEHVDPLHRRORALSAYSILITITOEQKFOEP 540

Qy 538 CFPCKNLASKYLVMDSPOMLCKIKVLRITMTDPTTELATITICIIINTVFLAVEHHNMD 597
Db 541 CFPCKNLASKYLVWECSPPLCIIKKVLOTMTDPTTELATITICIIINTVFLAVEHHNMD 600

Qy 598 DNLTKILKIGNWFTGIFIAECLKIIAIDPYHFRHGNVYFDSIVALLSLADLYNTLS 657
Db 601 NSLKDILKIGNWFTGIFIAECLKIIAIDPYHFRHGNVYFDSIVALLSLADLYNTLS 660

Qy 658 DNNRSFLASLRVLRVFLAKSWPTLNTLKIIGHSVGALGNLTVVLTIVFVSVGNRL 717
Db 661 -KNLSFLASLRVLRVFLAKSWPTLNTLKIIGHSVGALGNLTVVLTIVFVSVGNRL 719

718 FGTFENKTAYATQERPRRRHMDNFYHSFLVVRILCGEWIENMGCMQDMGSPLCIIV 777
Db 720 FGAFNKTC-STSPESLRWHMGDFYHSFLVVRILCGEWIENMGCMQDMGSPLCIV 778

Qy 778 FVLIMVIGKLVVNLFIALLNSFSNEBKDGSEGETRKTQVQLALDRFRRAFSPLMAL 837
Db 779 FVLIMVIGKLVVNLFIALLNSFSNEBKDGNEGETRKTQVQLALDRFRRAFSPLMAR 838

Qy 838 QSECCCKRRKNSPKPKETTESFAGENKDSILPDARPHKEYDTDMALTYGAGAPLAPLA 897
Db 839 QNFCCCKRRONSPKNEATESFAGESKDXDTATLDRSNKEXYDSEMTLYTGAGAPLAPLA 898

Qy 898 EVEDDVEYCGEGGALPTSOHSAVGQAGDLPPETTKQLTSPDDQGVMEVFESEDLHLSIQS 957
Db 899 KEEDDMCECCGDASPTSQPSEEAQCDLPLTKRLSPDDDHGVMEVFESEDPNLTIQS 958

Qy 958 PRKSDAVSMISECTIDLNDIFRNLOKTVSPKQDRCFPKGLSCHFLCHTKRKRSPW 1017
Db 959 ARKSDAASMLSECTIDLNDIFRNLOKTVSPKQDRCFPKGLSCHFLCHTKRKRSPW 1018

Qy 1018 VLWNNIRKTCYOIVKHSWFESFIIIVILLSSGALIFEDVNLPSRQVKKLLRCTDNITF 1077
Db 1019 VLWNNIRKTCYOIVKHSWFESFIIIVILLSSGALIFEDVNLPSRQVKKLLRCTDNITF 1078

Qy 1078 IFLLEMILKWAFGFRYFTSAWCWLDLIVVSVLSLMLNPLSKSFRTRLALRLRAL 1137
Db 1079 IFLLEMILKWAFGFRYFTSAWCWLDLIVVSVLSLMLNPLSKSFRTRLALRLRAL 1138

Qy 1138 QFEGKVVVYALISAIPALINLVLLVCLIFWLFCILGNLVNLSFGKFGRCINGTDINWLD 1197
Db 1139 QFEGKVVVYALISAIPALINLVLLVCLIFWLFCILGNLVNLSFGKFGRCINGTDINWLD 1198

Qy 1198 TEVNNRSOCNTSNYSWKYPQVNFNNGVGNAYLALLQVATYKGLWETMNAVDSREKDEPD 1257
Db 1199 SNVNPQSOCLVSNYTWKYPNFDNNGVGNAYLALLQVATYKGLWETMNAVDSRGDEQPA 1258

Qy 1258 FEANLYAYLYFVVFIFGSEFTNLNFIIGVIDNFNQOKKLGQDIFMTEBOKKYNYAMK 1317
Db 1259 FEANLYAYLYFVVFIFGSEFTNLNFIIGVIDNFNQOKKLGQDIFMTEBOKKYNYAMK 1318

Qy 1318 KLGTKKPKQIPRPLNKCAQFVDFLVTQVDFVILGLILVNLNMIIMAEASDAQDKVKKT 1377
Db 1319 KLGTKKPKQIPRPLNKCAQFVDFLVTQVDFVILGLILVNLNMIIMAEASDAQDKVKKT 1378

Qy 1378 FDILNIAFWLFTIECLIKVFALROHYFTNGWNLFDVCVVVLSIISTLVSRLESDISPP 1437
Db 1379 FDILNIAFWLFTIECLIKVFALROHYFTNGWNLFDVCVVVLSIISTLVSRLESDISPP 1437

Qy 1438 PTLFRVRLARIGRLRLVRAARGIRTLFALMMSLPSLNFNIGLLFLVMFYAIFGMSW 1497
Db 1438 PTLFRVRLARIGRLRLVRAARGIRTLFALMMSLPSLNFNIGLLFLVMFYAIFGMSW 1497

Qy 1498 FSKVKGSGIDDIINFNETFTGSMCLFOITTSAGWDTLNPNMLEAKEHCNSSQSCQOP 1557
Db 1498 FSKVKGSGIDDIINFNETFTGSMCLFOITTSAGWDTLNPNMLEAKEHCNSSQSCQOP 1557

Qy 1558 QIADVYFYSYIISPLIVNMVIAVLENFNATATESDPLGEDDFEFYEWKFDPEA 1617
Db 1558 QIADVYFYSYIISPLIVNMVIAVLENFNATATESDPLGEDDFEFYEWKFDPEA 1617

Qy 1618 SQFIQYSALSDFADALPEPLRVAKENKQFQLVMDLPMVWMDRLHCHMDVLFATTTVLGDS 1677
Db 1618 SQFIQYSALSDFADALPEPLRVAKENKQFQLVMDLPMVWMDRLHCHMDVLFATTTVLGDS 1677

Qy 1678 SGLDTMTKMEKFMENPFKLYEPIVTTTKRKEEEOGAAVIOYARKHMEKMKVLRUK 1737
Db 1678 SGLDTMTKMEKFMENPFKLYEPIVTTTKRKEEEOGAAVIOYARKHMEKMKVLRUK 1737

Qy 1738 DRSSSSHOVFCNGDLSLSDVAKVKVND 1765
Db 1738 GRSSSSHOVFCNGDLSLSDVAKVKVND 1765

```
RESULT 3
Q9JMD4 PRELIMINARY; PRT: 1765 AA.
ID Q9JMD4
AC Q9JMD4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created).
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT NAT/SCN1A.
GN SCN1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20090627; PubMed=10623609;
RA Ogata K., Jeong S.Y., Murakami H., Hashida H., Suzuki T., Masuda N.,
RA Hirai M., Ishihara K., Uchiyama Y., Goto J., Kanazawa I.;
RT "Cloning and expression study of the mouse tetrodotoxin-resistant
RT voltage-gated sodium channel alpha subunit Nat/Scn1a.";
RL Biochem. Biophys. Res. Commun. 267:271-277(2000).
DR EMBL; AB031389; BAA92154.1; -.
DR MGI; MGI:1345149; Scn1a.
DR InterPro; IPR000636; Cation_chan_nlig.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1765 AA; 201305 MW; FFF1D121CB9C6DA CRC64;

Query Match 88.1%; Score 8085; DB 11; Length 1765;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1560; Conservative 95; Mismatches 107; Indels 6; Gaps 5;

Qy 1 MEERYPVIFPDERNFRFTSDSLAAIKKRIATQKERKSKDKAAAEQPPRPQLDLKASR 60
Db 1 MEERYPVIFPDERNFRFTSDSLAAIEKRITQEKKKSKDKAAATEQPPRPQLDLKASR 60
Qy 61 KLPKLYGDIPPELVTKPLEDDPYKHKTFWLNKKTTFYRFSAKRALFILGPNPLRS 120
Db 61 KLPKLYGDVPPDLTAKPLEDDPYKHKTFWLNKKTTFYRFSAKRALFILGPNPLRS 120
Qy 121 LMIRISVHSVSMFTICTVIINCMFMAN--SWERSFDNDIPEYFYGIIYLEAVIKILAR 178
Db 121 FMIRISVHSVSMFTICTVIINCMFMANSSVDSRPPSSNIPEYFYGIIYLEAVIKILAR 180
Qy 179 GFIVDEFSFLRDPNNWLDVIFVIGTAIATCFPGSQV-NLSALRTFRVFRALKAISVISGLK 237
Db 181 GFIVDEFSYLRDPNNWLDVIFVIGTAIAPCFLGNKVNLSLTLRTFRVLRALKAISVISGLK 240
Qy 238 VIVGALLRSVKLVDMVWLTFLFCLISFALVGOQLFMGLINOKCIKHNGCPNPASKDCFE 297
Db 241 VIVGALLRSVKLVDMVWLTFLFCLISFALVGOQLFMGLTSQKCKDDCGPNAFNKKDCFV 300
Qy 298 KEKSEDFIMCGTWLGRPCPNSTCDKTTLNPDNNYTKFDFNGWSFLAMFRVMTQDSWE 357
Db 301 KENSEDFIMCGNWLGRSCPDGCTCKTTNPDNYTNFDSFGWSFLAMFRVMTQDSWE 360
Qy 358 KLYRQLRTSGIYFVFVFFVIFGSGFYLLNLTAVVTMAYEQNRNVAATEAKEKMFQ 417
Db 361 KLYRQLRTSGIYFVFVFFVIFGSGFYLLNLTAVVTMAYEQNRNVAATEAKEKMFQ 420
Qy 418 EAQQLLREEKALVAMGIDRRSLNSLQASSFPKKRFFGSKTRKSPFMRGSKTAQASAS 477
Db 421 EAQQLLREEKALVAMGIDRTSLNSLQASSFPKKRFFGSKTRKSPFMRGSKTARASAS 480
Qy 478 DSEDDASKNPOLLEQTKRLSQNLPVDFDEHVDPLHQRALSAVSILTTITQEQEKFOEP 537
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481 DSEDDASKNPOLLEQTKRLSQNLPVDFDEHVDPLHQRALSAVSILTTITQEQEKSQEP 540
Qy 538 CFPCKGNLASKYLVWDCSPQWLCKIKKVLRTIMTDFTTELATICTIIINTVFLAVEHNMND 597
Db 541 CFPCKGNLASKYLVWDCSPQWLCKIKKVLQTIMTDFTTELATICTIIINTVFLAMEHNMND 600
Qy 598 DNLKTILKIGNWFTGIFIAECLKIIALDPHYHFRHGNVFDLSIVALLSLADLYNTLS 657
Db 601 NSLKDILKIGNWFTGIFIAECLKIIALDPHYHFRHGNVFDLSIVALLSLADLYFHLS 660
Qy 658 DNNRSLASLRVLRVFKLAKSNPTLNTLIKIIHGSVGALGNLTIVVLTIVVFVVGMRLL 717
Db 661 -KNLSFLASLRVLRVFKLAKSNPTLNTLIKIIHGSVGALGNLTIVVLTIVVFVVGMRLL 719
Qy 718 FGTGFENKATAYATQERPRRRHMDNFYHSFLVVFRILCGEWENMMGCMQDMGSPCLICIV 777
Db 720 FGAENKTCSTSPESLRRR-HMGDFYHSFLVVFRILCGEWETWMDCMQEMEGSPCLCIV 778
Qy 778 FVLINVIKLVNLFIALLNFSNEEKDGSLEGETRKTQVQLALDRFRRAFSMLHAL 837
Db 779 FVLINVIKLVNLFIALLNFSNEEKDGNPEGETRKTQVQLALDRFRSRAFYEMARAL 838
Qy 838 QSFCKCKRRKNSPKPKETTESFAGENKDSILPDARPKKEYDTDMALYTGQAGAPLAPLA 897
Db 839 QNFCKRCKRRQNSPKPNEATESFAGESRDTATLDRSNKEYDSEMTLYTGQAGAPLAPLA 898
Qy 898 EVEDDVYCGEGGALPTSOHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQS 957
Db 899 KEEDDMCECCGDSAPTSQPSAEQAQCDLPLKTKRLPSDDHGVEMEVFSEEDPNLTIQS 958
Qy 958 PRKKSDAVSMISECSTIDLNDIFRNLOKTVSPKQDPDRCFPKGLSCHFLCHTKDRKSPW 1017
Db 959 ARKKSDAASMLSECSTIDLNDIFRNLOKTVSPKQDPDRCFPKGLSCIFLCKCTIRKKSPW 1018
Qy 1018 VLWNIRKTCYQIVKHSWFESFIFVILLSSGALLFEDVNLPSRPQVEKLLRCTNITTF 1077
Db 1019 VLWNIRKTCYQIVKHSWFESFIFVILLSSGALLFEDVNLPSRPQVEKLLRCTNITTF 1078
Qy 1078 IFLLEMLILKLVAFGRYFTSAWCMLDFLIVVSVLSLMLNPSLKSFRTLRALRPLALS 1137
Db 1079 IFLLEMLILKLVAFGRYFTSAWCMLDFLIVVSVLSLMLNPSLKSFRTLRALRPLALS 1138
Qy 1138 QFEGMKVVYALISAIPAILANVLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDF 1197
Db 1139 QFEGMKVVYALISAIPAILANVLVCLIFWLVFCILGVNLFSGKFGRCINGTDINKYFNA 1198
Qy 1198 TEVNRSCNISNYSWKVPQVNFQNGVAYLALQVATYKGLWELMNAVDSREKDEQPD 1257
Db 1199 SNVPMOSCLYSNHTWKVPNVNFQNGVAYLALQVATYKGLWELMNAVDSRGDEQPA 1258
Qy 1258 FEANLYAYLVFVFTIFGSFNTLNFIGVIDNFNQOQKLGQDIFMTEQKKYYNAMK 1317
Db 1259 FEANLYAYLVFVFTIFGSFNTLNFIGVIDNFNQOQKLGQDIFMTEQKKYYNAMK 1318
Qy 1318 KLGTKKPKPIPRPLNKCOAFVFDLVTSQVFDVILGLILVNLMIIMMAESADOPKDKVT 1377
Db 1319 KLGTKKPKPIPRPLNKCOAFVFDLVTSQVFDVILGLILVNLMIIMMAESADOPKDKVT 1378
Qy 1378 FDILNIAFWITTECLIKVFAIRQHYFTNGNLFDCVWVLSIISTLVSRLEDDSDIGFP 1437
Db 1379 FDILNIAFWITTECLIKVFAIRQHYFTNGNLFDCVWVLSIISTLVSRLEDDSDIGFP 1437
Qy 1438 PTLFRVRLARIGRLRLVRAARGIRTLFALMMSLPSLFNIGLLFLVMFYIAIFGMSW 1497
Db 1438 PTLFRVRLARIGRLRLVRAARGIRTLFALMMSLPSLFNIGLLFLVMFYIAIFGMSW 1497
Qy 1498 FSKVKGSGIDDDIENFETFTGSMCLFOITTSAGNDTLLNPMLEAKEHCNSSSQSCQOP 1557
Db 1498 FSKVKGSGIDDDIENFETFTGSMCLFOITTSAGNDTLLNPMLEAKEHCNSSSQSCQOP 1557
Qy 1558 QIAYVYFVYTIISPLIVNMVYIAVILENFNTATSESDPLCEDDFFEIFYVWEKFDPEA 1617
Db 1558 QIAYVYFVYTIISPLIVNMVYIAVILENFNTATSESDPLCEDDFFEIFYVWEKFDPEA 1617
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Db 1558 QIAIYVFSYIIISLLIIVNMYIAVILENFNTATSESDPLGEDDFEIPFYEIWEKFDPEA 1617
Qy 1618 SOFIQYSALSDFADALPEPLRVAKPNKQFQFLVMDLPVMYMGDRHLHMDVLFAPFTTRVLGDS 1677
Db 1618 TOFIQYSALSDFADALPEPLRVAKPNKQFQFLVMDLPVMYMGDRHLHMDVLFAPFTTRVLGDS 1677
Qy 1678 SGLDTMKTMKEEKFMEANPFKLYPIVTTTKRKEEBEAGAAVIOQARYAKHMEKWKVLRK 1737
Db 1678 SGLDTMKTMKEEKFMEANPFKLYPIVTTTKRKEEBEAGAAVIOQARYAKHMEKWKVLRK 1737
Qy 1738 DRSSSSHOFVFCNGDLSLSDVAKVKVHND 1765
Db 1738 GRSSSLQVFCNGDLSLSDVPAIKVHCD 1765
RESULT 4
Q9UI33 PRELIMINARY; PRT: 1791 AA.
ID Q9UI33
AC Q9UI33;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT SCN12A.
GN SCN12A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20090626; PubMed=10623608;
RA Jeong S.-Y., Goto J., Hashida H., Suzuki T., Ogata K., Masuda M.,
RA Hirai M., Isahara K., Uchiyama Y., Kanazawa I.,
RT "Identification of a novel human voltage-gated sodium channel alpha
RT subunit gene, SCN12A.";
RL Biochem. Biophys. Res. Commun. 267:262-270(2000).
DR EMBL: AF109737; AAF24976.1;
DR InterPro: IPR000636; Cation_chan_non_lig.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001696; Na_channel.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR Pfam: PF00520; Ion_trans; 4.
DR PRINTS: PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1791 AA; 204947 MW; E85D3E790E141D068 CRC64;

Query Match 73.2%; Score 6714; DB 4; Length 1791;
Best Local Similarity 72.9%; Pred. No. 0;
Matches 1316; Conservative 178; Mismatches 258; Indels 52; Gaps 14;

Qy 1 MEERYVPVFPDERNFRFTSDSLAAIKRTAIQKERRKSKDKAAAEQPRQLODKASR 60
Db 1 MDDRCYVFPDERNFRFTSDSLAAIEKRTAIQKERRKSKDKQDQGEVQPRQLODKASR 60
Qy 61 LKPLKLYGDIPLVTKPLEDDPYKDKHTFMVLNKKRTIYRFSAKRALFILGPNPLRS 120
Db 61 LKPLKLYGDIPLVTKPLEDDPYKDKHTFMVLNKKRTIYRFSAKRALFILGPNPLRS 120
Qy 121 LMIRISVHSVSMFICTVIINCMPMANSMER--SFNDPIPEYVFIGIYILEAVIKILA 177
Db 121 LAIRYSVHSVSMFICTVIINCMPMANSMER--SFNDPIPEYVFIGIYILEAVIKILA 180
Qy 178 RGFIVDESFLRDPNNWLDVIFVIGTAIATCPGSGOVNISALRTFRFRALKAISVIGLK 237
Db 181 RGFILDEFSFLRDPNNWLDVIFVIGTAIATCPGSGOVNISALRTFRFRALKAISVIGLK 240
Qy 238 VIVGALLRSVKLVDMVLTFLCISIFALVGOOLPMWILNOKCIKHNCG--PNPASNDC 295
Db 241 VIVGALLRSVKLVDMVLTFLCISIFALVGOOLPMWILNOKCIKHNCG--PNPASNDC 300
Qy 296 FEKEKDSDFIMCGTWLGRPCNGSTCDKTTLPNDNNYTKTFDNLFGWSFLAMFRVMTQDS 355

Db 301 FEKENSPEFKCGIWMGNSACSIOYECKHTKINPDYNTNFDNFGWSFLAMFRVMTQDS 360
Qy 356 WERLYRQILRTSGIYVFFVVFVIFLGSFYLLNLAVVTMAYEQNRNVAETAKEM 415
Db 361 WEKLYQQILRTTGLSVFFVIFLGSFYLLNLAVVTMAYEQNRNVAETAKEM 420
Qy 416 FOEAQOQLREKEALVAMGIDRSSLSQASSFSFKKFFGSKTKRFFFMGRGSTAQAS 475
Db 421 FOEAQOQLREKEALVAMGIDRSSLSQASSFSFKKFFGSKTKRFFFMGRGSTAQAS 480
Qy 476 ASDDEDDASKNPOLLEOTKRLSONLPVLDLFDHVDPLHQRALSAVSILTIQOEKQ 535
Db 481 GSDSDEDCQKPOLLEOTKRLSONLPVLDLFDHVDPLHQRALSAVSILTIQOEKQ 540
Qy 536 EPCFPCGKNLASKYLWDCSPOWLCTIKVLRITMDPTTELAIITCIINTVFLAVEHNN 595
Db 541 EPCFPCGKNLASKYLWDCSPOWLCTIKVLRITMDPTTELAIITCIINTVFLAVEHNN 600
Qy 596 MDDNLKTLKIGNWVFTGIFIAEMCLKIADLPYHYFRHGMVDFSIALLADLVNT 655
Db 601 MEASPEKMLNIGLVFTSIFIAEMCLKIADLPYHYFRHGMVDFSIALLADLVNT 660
Qy 656 LSDNRSFLASLVRVLFKLAKSWPTLNTLKIIGHSVAGLGNLVLTVIVFISVVG 715
Db 661 LQKRSWPLRSRVLRFKLAKSWPTLNTLKIIGHSVAGLGNLVLTVIVFISVVG 720
Qy 716 RLFGTKENKATAYATQERPR-----RRWMDNPFYHSFLVVFRTLCGGEWENMWG 763
Db 721 QLFGRSFN-----SOKSPKLCNPTGTVSCLRHWMGDFWHSFLVVFRTLCGGEWENMWG 775
Qy 764 CMQDMQD-GSPLCIIIVFLIMVIGKLVNLFALLNLSFNEEKDGLSEGETKRTKVQLA 822
Db 776 CMQEANASSLGVIFILLITVIGKLVNLFALLNLSFNEEKDGLSEGETKRTKVQLA 835
Qy 823 LDRFRRAFSLMALQSCCKKCRKNKSPKPKETTESFAGENKDSILP---DARPMKEYD 879
Db 836 LDRFRRAFSLMALQSCCKKCRKNKSPKPKETTESFAGENKDSILP---DARPMKEYD 894
Qy 880 TDMALYTGQAGAP-----LAPLAEEVDDVEYCEGEGALPTSOHSAGVQAGDLP 928
Db 895 EELGILT---SVPKTLGVNHDWTLAPLAEEVDDVEYCEGEGALPTSOHSAGVQAGDLP 951
Qy 929 ETQKLTSPDDQGVEMEVFSEEDLHLSIQSPRKSDAVSMLESCSTIDLNDIFRNKQTSV 988
Db 952 ENKKTQSQRVQSVDEIDMFSEDEPHLTIQPRKSDVTSILSECSSTIDLDGQGNLPEMV 1010
Qy 989 PKQPDRCPPKGLSCHFLCHKTKDRKSPVLMNIRKTCYQIVKHSWFESFIIFVILLSS 1048
Db 1011 PKQPDRCPPKGLSCHFLCHKTKDRKSPVLMNIRKTCYQIVKHSWFESFIIFVILLSS 1070
Qy 1049 GALIFEDVNLPSRPOVEKLLRCTDNITFTIFILEMLKWAAGFRFRYFSAWCLDFLIV 1108
Db 1071 GALIFEDVNLPSRPOVEKLLRCTDNITFTIFILEMLKWAAGFRFRYFSAWCLDFLIV 1130
Qy 1109 VVSVLNMLNPLSKFRTRLRALRALSOFGCMKVYVALISAIPAILNVLVCLIFWL 1168
Db 1131 IVSVVTLLNMLKFRTRLRALRALSOFGCMKVYVALISAIPAILNVLVCLIFWL 1190
Qy 1169 VFCILGVNLFSGKFGRCINGTIDINMYLDFTEVPNRSQCINISNYSWKVPQVNDVGNAYL 1228
Db 1191 VFCILGVNLFSGKFGRCINGTIDINMYLDFTEVPNRSQCINISNYSWKVPQVNDVGNAYL 1248
Qy 1229 ALLQVATYKGLWEINNAVDSREKQDPDEANLAYLVFVYVFIIFGSEFTNLNLFIV 1288
Db 1249 ALLQVATYKGLWEINNAVDSREKQDPDEANLAYLVFVYVFIIFGSEFTNLNLFIV 1308
Qy 1289 DNFNQOQKLGQDIFMTEEQKYYNAMKLGCTKPKQPIPRPLANKCAQAFVLDVTSQVF 1348
Db 1309 DNFNQOQKLGQDIFMTEEQKYYNAMKLGCTKPKQPIPRPLANKCAQAFVLDVTSQVF 1368
Qy 1349 DVIIIGLIVLNMIIMAESADQPKDKKTDILNIAFVIFVIFTECLIKVFLARQHYFTNG 1408
Db 1408 DVIIIGLIVLNMIIMAESADQPKDKKTDILNIAFVIFVIFTECLIKVFLARQHYFTNG 1408

Db 1369 DIIIIISLIILNISMMAESYNOPKAMKSILDLNWNVVFVITLECLIKIFALRQYVFTNG 1428
 QY 1409 WNLFCVWVVLSTIISTVLSRLSDS- ISFPPTLFRVRLARIGRILRLVRAARGITLLF 1467
 Db 1429 WNLFCVWVVLSTIISTVLSRLSDS- ISFPPTLFRVRLARIGRILRLVRAARGITLLF 1488
 QY 1468 ALMMSLPSLFTNIGLGLLFLVMFYAIFGMSWFKVKGSGIDIDIFNFETPGSMCLCFQIT 1527
 Db 1489 ALMMSLPSLFTNIGLGLLFLVMFYAIFGMSWFKVKGSGIDIDIFNFETPGSMCLCFQIS 1548
 QY 1528 TSAGWDTLLNPMLEAKHCNCSQSQCOQPIAVYFVYSYIIISFLIVVMYIAVILENF 1587
 Db 1549 TSAGWDTLLNPMLEAKHCNCSQSQCOQPIAVYFVYSYIIISFLIVVMYIAVILENF 1607
 QY 1588 NTATESEDPGLCEDDFEYFVWEKFDPEASQFIQYSALSDPADALPEPLRVAKPNKQF 1647
 Db 1608 NTATESEDPGLCEDDFEYFVWEKFDPEATQFIKYSALSDPADALPEPLRVAKPNKQF 1667
 QY 1648 LVMDLPVMYMGDRHLHGMVLFVFTTRVLGDSGLDTMTKMTMEKFEANPFKKLYEPIVTT 1707
 Db 1668 LVMDLPVMYMGDRHLHGMVLFVFTTRVLGDSGLDTMTKMTMEKFEANPFKKLYEPIVTT 1727
 QY 1708 TKRKEEGCAAVIQRAYRKHMKMYKLRLKDRSS-----SSHQVFCNGDLSLSDVAKVK 1761
 Db 1728 TKRKEEGCAAVIQRAYRKHMKMYKLRLKDRSS-----SSHQVFCNGDLSLSDVAKVK 1787
 QY 1762 VHND 1765
 Db 1788 VHCD 1791

RESULT 5

Q0UHE0 PRELIMINARY; PRT: 1791 AA.
 AC Q0UHE0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE VOLTAGE-GATED SODIUM CHANNEL TYPE XI ALPHA SUBUNIT.
 GN SCN1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=DORSAL ROOT GANGLIA;
 RX MEDLINE=20047838; PubMed=10580103;
 RA Dib-Hajj S.D., Tyrrell L., Cummins T.R., Black J.A., Wood P.M.,
 RA Waxman S.G.;
 RT "Two tetrodotoxin-resistant sodium channels in human dorsal root
 ganglion neurons";
 RL FEBS Lett. 462:117-120(1999).
 DR EMBL; AF188679; AAF17480.1; -.
 DR InterPro; IPR000636; Cation_chan_non_lig.
 DR InterPro; IPR001682; Channel_pore_Ca_Na.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR Pfam; PF00520; Ion_trans; 4.
 DR PRINTS; PR00170; NACHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 1791 AA; 204920 MW; DE38680BFB639ED1 CRC64;

Query Match 73.18; Score 6709; DB 4; Length 1791;
 Best Local Similarity 72.9%; Pred. No. 0;
 Matches 1315; Conservative 179; Mismatches 258; Indels 52; Gaps 14;
 QY 1 MEERYYPVFPDPERFRFTSDSLAAIKKRTAIQKERRKSKDKAAAEQPPQOLDKASR 60
 Db 1 MDDRCYPVFPDPERFRFTSDSLAAIKKRTAIQKERRKSKDKQDTEVQPPQOLDKASR 60
 QY 61 KLPLKLYGDIPELVTKPLEDDLPYKDKHKTFLMVLNKRRTIYRFSAKRALFILGPFNPLRS 120

Db 61 KLPLKLYGDIPELVTKPLEDDLPYKDKHKTFLMVLNKRRTIYRFSAKRALFILGPFNPLRS 120
 QY 121 LMRISVHSVSMFICTVIINCMFMANSMER---SFDNDIPEYVFIGIYILEAVIKILA 177
 Db 121 LAIRSVHSLSFWMFICTVIINCMFMANSMER---SFDNDIPEYVFIGIYILEAVIKILA 180
 QY 178 RGFIVDESFLLDPNWNLDVFIIVGTATATCFPGSQVNLALRTFRFRALKAISVLSGLK 237
 Db 181 RGFILDEFSLDPNWNLDVFIIVGTATATCFPGSQVNLALRTFRFRALKAISVLSGLK 240
 QY 238 VTVGALLRSVKLVDMVLTFLCLSFIFALVGQOLFGLMILNOKCIKHNGC--PNPASNKDC 295
 Db 241 VTVGALLRSVKLVDMVLTFLCLSFIFALVGQOLFGLMILNOKCIKHNGC--PNPASNKDC 300
 QY 296 FEKEDSEDFIMCGTWLGRPCPNSTCDKTTLPNDNNYTKFDNFGWSEFLAMFRVMTQDS 355
 Db 301 FEKEDSEDFIMCGTWLGRPCPNSTCDKTTLPNDNNYTKFDNFGWSEFLAMFRVMTQDS 360
 QY 356 WERLYRQILRTSGIYFVFFVVFVIFLGSFYLLNLTLAVTVMAYEQNRNVAATEAKEM 415
 Db 361 WEKLYQOTLRTTGLYVFFVVFVIFLGSFYLLNLTLAVTVMAYEQNRNVAATEAKEM 420
 QY 416 FOEAQOLLREKEALVAMGIDRSSLSLQASSFPKRRKFFGSKTRKSFMRGSKTAQAS 475
 Db 421 FOEAQOLLREKEALVAMGIDRSSLSLQASSFPKRRKFFGSKTRKSFMRGSKTAQAS 480
 QY 476 ASDDDASKNPQLLEQTKRLSONLPVDLFDHVDPLHQRALSAVSILITIQBOEKFO 535
 Db 481 GSDSDCQKPKQLLEQTKRLSONLPVDLFDHVDPLHQRALSAVSILITIQBOEKFO 540
 QY 536 EPCFPGKNLASKYLWDCSPQWLCIKKYLRTIMTDPPTLTAITICIIINTVFLAVEHIN 595
 Db 541 EPCFPGKNLASKYLWDCSPQWLCIKKYLRTIMTDPPTLTAITICIIINTVFLAVEHIN 600
 QY 596 MDDNLTKILIGNWVFTGIFIAEMCLKIITADLPYHFRGWNVDFSIALLSLADLYNT 655
 Db 601 MEASFEMKLNIGNVFTSIFIAEMCLKIITADLPYHFRGWNVDFSIALLSLADLYNT 660
 QY 656 LSDNRSFLASURVLRVFKLAKSWPTNLTKIIGHSVAGALNLTVVLTVIVFISVVG 715
 Db 661 LOKRWPFLSRVLRVFKLAKSWPTNLTKIIGHSVAGALNLTVVLTVIVFISVVG 720
 QY 716 RLFGTKFNKTAVATQERPR-----RRWMDNFYHSLVVRILTCGGEWENMG 763
 Db 721 QLFGRSFN-----SOKSPKLCNPTGPTVSCLRHWHMGDFHSLVVRILTCGGEWENMG 775
 QY 764 CQMDMD-GSPLCIIVFIMVIGKLVNLFALLNSFNEEKDGSLGEGTRKTKVQLA 822
 Db 776 CQMDMD-GSPLCIIVFIMVIGKLVNLFALLNSFNEEKDGSLGEGTRKTKVQLA 835
 QY 823 LDRFRRAFSLHALQSCCKKCRKNKSPKKTETTESFAGENKDSILP---DARPMKEYD 879
 Db 836 LDRFRRAFSLHALQSCCKKCRKNKSPKKTETTESFAGENKDSILP---DARPMKEYD 894
 QY 880 TDMALYTGQAGAP-----LAPLAEVDEDDVEYCGEGGALPTFSQHSAGVQAGDLPP 928
 Db 895 EELGILT---SVPKTLGVHRHDMTWLAPLAEVDEDDVEYCGEGGALPTFSQHSAGVQAGDLPP 951
 QY 929 ETQKLTSPDDQGVMEVESEEDLHLSIQSPRKKSDAVSMLSECSTIDLDIFRNLTQKTVS 988
 Db 952 ENKKTSPQRVQSVEDIMFSEDEPHLTIQDPRKSDVTSILSECSTIDLDGFGWLPDMV- 1010
 QY 989 PKQDPRDFPKGLSCHFLCHTKDKRKSPPVLMWNRKTCYQIVKHSWFSFIFVILLSS 1048
 Db 1011 PKQDPRDFPKGLSCHFLCHTKDKRKSPPVLMWNRKTCYQIVKHSWFSFIFVILLSS 1070
 QY 1049 GALIPEDEVNLPSPQVEKLLRCTDNIFTFIFLEMLTKWAFGRFYFTSACWLDLFLV 1108
 Db 1071 GALIPEDEVNLPSPQVEKLLRCTDNIFTFIFLEMLTKWAFGRFYFTSACWLDLFLV 1130
 QY 1109 VYVSLSLMNLPSLKSFRTLRLRPLRALSOFEGCMKVVVVALISAPAILNVLVLFWL 1168

Db 895 BELGILT---SVPKTLGVHRDWTWLAFLAEEEDDVEFSGEDNAORITQPEQOAYELHQ 951

Qy 929 ETQKLTSPDDQGVEMEVESEEDLHLSIQSPRKSDAVSMLSECSTIDINDLFRNLQKTVS 988

Db 952 ENKPTSORVOSVEIDMESEDEPHLTQIDPRKSKDVTSLSECSTIDLDQDGFGLPEWV- 1010

Qy 989 PKKQDRCPFKGLSCHFHCTDKRSPWLNWNRKTCYQIYVHSHWSEFIIFFVILLSS 1048

Db 1011 PKKQERCLPKGFCGCCFCCSVDRKPKPWVWNLNRKTCYQIYVHSHWSEFIIFFVILLSS 1070

Qy 1049 GALIFEDVNLSPRQVEKLLRCDTNIFFIFLLEMLKWAFAFGFRYFTSAMCWLDLIV 1108

Db 1071 GALIFEDVHLENQPKIOELLNCTDIIFTHIFLEMLKWAFAFGFKYFTSAMCCLDFIIV 1130

Qy 1109 VSVLSLNLPLSLKSFRTLRALRALSOFEGMKVWVYALISATPALNVLVCLIFWL 1168

Db 1131 IVSVTTLNLMELKSFRTLRALRALSOFEGMKVWVYALISATPALNVLVCLIFWL 1190

Qy 1169 VFCILGVNLFSGKFGKRCINGTDINMYLDFTEVPNRSCQNI SNYMKVPQVNFNDVGNAYL 1228

Db 1191 VFCILGVYFSGKFGKRCINGTD--SVINYTIITNKSQCESGNFWSHNGKVFNDVGNAYL 1248

Qy 1229 ALLQVATYKGMLEIMNAADVREKDEQDPDEANLYAYLYFVYFIIFGFFFTLNFIGVII 1288

Db 1249 ALLQVATEKGWMDIYAAVDSTEKQBQPEFESNSLYFYFVYFIIFGFFFTLNFIGVII 1308

Qy 1289 DNFNOQKKGODIFMTTEOKKYNNAMKLGTKPKQPIRPLNCKOAFVFDLVTQVF 1348

Db 1309 DNFNOQKKGODIFMTTEOKKYNNAMKLGSKPKQPIRPLNCKOGLVFDIVTSQIF 1368

Qy 1349 DVITLGLVLNMIIMAESADQKDKVTKFDLNTAFVVIETIECLIKVFAALRQHYFTNG 1408

Db 1369 DIIITSLILNIMSMAESYNQPKAMKSILDHLNWFVVIETIECLIKIIPALRQHYFTNG 1428

Qy 1409 WNLFCVWVLSIIS 1423

Db 1429 WNLFCVWVLSIIS 1443

RESULT 7

Q9JJV9 PRELIMINARY; PRT; 2019 AA.

AC Q9JJV9;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE VOLTAGE-GATED SODIUM CHANNEL.

GN SCN5A.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C; TISSUE=HEART;

RA Zimmer T., Beandorf K.;

RT "the mouse heart sodium channel (mhl): cloning and characterization of

RT alternatively spliced variants.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ271477; CAB70096.1; -.

DR MGD; MGI:98251; Scn5a.

DR InterPro; IPR000536; Cation_chan_non_lig.

DR InterPro; IPR002111; Cat_channel_Trbp.

DR InterPro; IPR001682; Cat_channel_Pore_Ca_Na.

DR InterPro; IPR000048; IQ.

DR InterPro; IPR001696; Na_channel.

DR Pfam; PF00520; ion.trans. 4.

DR Pfam; PF00612; IQ; 1.

DR PRINTS; PR00170; NACHANNEL.

DR SMART; SM00015; IQ; 1.

KW Ionic channel.

QY SEQUENCE 2019 AA; 227620 MW; FDB48750D599B89A CRC64;

Query Match 51.6%; Score 4730; DB 11; Length 2019;

Best Local Similarity 50.1%; Pred. No. 0;

Matches 976; Conservative 286; Mismatches 423; Indels 262; Gaps 32;

Qy 15 NFRPFTSLAAIKKRIAIQKER-----KSKDKAAAEPPQRPQDLQKASRKLPLKLYGDI 69

Db 12 SFRRTRESLAIEKRAEAKQARGSATQSESEGLPEEAPRPQDLQKASRKLPLKLYGDI 71

Qy 70 PPELVTKPLEDLDPPYKDKHTFMVNLKRTIYRFSAKRALFGLFPNPLRSLRIMIRISVHS 129

Db 72 PRELIGEDLDPPYSTQKTFIVLNKGTIFRFSATNALYVLSFHPVRRAAVILVHS 131

Qy 130 VFSFELICTVIINCMFANSMERSFDNDIP-----EYFVGIIYLEAVIKILARGFIVD 183

Db 132 LFSMLIMCTIITNCVFMA-----OHDPPTWKYVETFTYTAIYTFESLVKILARGFCLH 184

Qy 184 EFSFLRDPNNWLDFTVIGTAIATATCPGSGVNLSSALRTRFRVFRALKAISVISGLKIVGAL 243

Db 185 AFTFLRDPNNWLDFTSVIVWAYTEFV-DLGNVSALRTRFRVLRALAKTIVISGLKIVGAL 243

Qy 244 LRSVKVLVDVWVLTFLCLISIFALVGOQLFMGLLNOKCIKHNC-----GNPASHKD----- 294

Db 244 IQSVKKLADVWVLTFLCLISVFALIGLQFMGNLRHKVNRFTELNGTNGSVEADGIVWNS 303

Qy 295 -----CFEKEKDEDFIMCGTWLGSRPCNGSTCDKTTLNPDNNYTKFDNFGWFL 345

Db 304 LDVYNDPANVLLKNGTDDVLLCGNSDAGTCPEGYRCLKAGENPDHGTSTFSDSAWAF 363

Qy 346 AMFRVMTQDSWERLYRQILRTSGIYFVFFVVFVIFGLSYFLNLTLAVVTWAYEYQNRNV 405

Db 364 ALFRMTQDWERLYRQILRTSGIYFVFFVVFVIFGLSYFLNLTLAVVTWAYEYQNRNV 423

Qy 406 AAETAEKMFQEAQOLLREEKEALVANGIDRSSNLNSIQASSFS------KKRKTFG 457

Db 424 IAEETEEKRQEAAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNTNHERSKRKL 483

Qy 458 SKT-----RKSFFMRGSKTA-----QASASDS 479

Db 484 SGTEGDDGDRLPKSDSEDPALNOLSLTHGLSRTSMPRSRSGSITFTFRRDQGEADF 543

Qy 480 EDDASK----- 485

Db 544 ADDENSTAGESHRTSLVWPWLPRLRPSTQGPFGTSGPHGVNLGNKRNSTVDCNVVSL 603

Qy 486 -----NFOLEQ-----TKRLSNLP-VDLFDHVDPLHRQ 515

Db 604 LGAGDAEATSPGSHLLRPVLDLPPDTTTPSEPGPQMLTPQAPCAGDFEE---PGARQ 660

Qy 516 RALSAVSLTITIQEKEFPQPCPGKNLASKYLWDCSPQWLCKIKKVLRTIMTDPTE 575

Db 661 RALSAVSLTSALEESHRKCPPCWNRFAQHYLIWECCPLMWSIKQKVFVMDPFAD 720

Qy 576 LAITICIINTVFLAVEHNNDDNLTKLTIGNWVFTGIFIAEMCKIILADPYHYFRHG 635

Db 721 LTIFWCVLNTLFALEHYNTAEFEMLQVGNLVFTGIFTAEMTKIILADPYHYFOG 780

Qy 636 WNVFDSIIVALLSLADVLYNTLSDNNRSLASLRVLRVFKLAKSWPTLNTLIKIIGHSYGA 695

Db 781 WNVFDSIIVALLSLADVLYNTLSDNNRSLASLRVLRVFKLAKSWPTLNTLIKIIGHSYGA 838

Qy 696 LGNLTIVLVTVFVPSVVGMLRFGTKFNKTAYATQER---PRRRWHMDFYHSLFVFPRI 752

Db 839 LGNLTIVLVTVFVPSVVGMLRFGTKFNKTAYATQER---PRRRWHMDFYHSLFVFPRI 896

Qy 753 LCGEWIENWGMQMDGSPICIIIVFLIMVIGKLVNLFTALLNLSFSNE-----BKD 807

Db 897 LCGEWIETWDCM-EVSCQSCLLVVLLVWVIGNLVNLFLUALLLSFSFADNLTPADEP 955

Qy 808 GSLEGETRKTQVQALDRFRRAFSFMLHALQSFCCCKCRK----- 848

Db 956 GEM-----NNLQALARIQGLRFVKRTTWDTCGGLLRRRPPKPAALATHSQLPSCITT 1009

Db 532 SHRSLLLGGAGGAGGQGLPRSPLOPSPNDPSRGEDEHQPPP-----TSELAPGADVSA 586
Qy 505 PD-----EHDV-D-PLHQRALSAVSILITIQEOEKQEPQPCGKKNLASKYLYWD 553
Db 587 FDAGOKKTFLSNEYDEDFRAQRAMSVSIISVLEESQKPPCLTSLSQKYLWD 646
Qy 534 CSPQWLCKIKVLRITMTDPTTELATITICIIINTVLAHEHNMDDNLTKILKIGNVFTG 613
Db 647 CCPMVKLKTILFGLVTPDPAELTITLCIVVNTIFMAHEHGMSPTEAMLIQIGNIVTI 706
Qy 614 IFIAEMCLIKIALDYPHYFRGHWVFDISVALLSLADVLYNTLSNNRSFSLASLVRVF 673
Db 707 FFAEMVFKIIAFDPIYFFQKWNFIIDCIITVTSLEL--GVAKGKGLSVLRSPFLLRVF 764
Qy 674 KLAWSPTLNTLIKTIHGSVAGLNLTVLTIIVFISVGMRLFGTKF--NKTAYATOE 731
Db 765 KLAWSPTLNTLIKTIHGSVAGLNLTIILAIIVFVAGLQKLLGENYRNNKNISAPH 824
Qy 732 RPRRHHMDFHSPVFRILCGEWIENMGCMODGSPLCIIVFVLINWIGKLVVLN 791
Db 825 EDWPRHHMDFHSPVFRILCGEWIENMACM--EVGKSCICILILFLTVWVGLNVLN 883
Qy 792 LFIALLLNSFNE-----EKDGLSEGETRKTQVQALDRFRRAFSFMLHALOSFCKRCR 846
Db 884 LFIALLLNSFADNLTAPEDDGEV-----NNLQVALARIOVFGHRTQOALCSFPRSQ- 936
Qy 847 RKNSPKPKETTE-----SFAGEN-----KDSILPDARPKWEYDMDALYTQ 888
Db 937 --PPQPKRAEPVLVVKLPLSSKKAENHIAANTARGSSGLOAPRDRDEHSDFIANPTVW 994
Qy 889 AGAPLA-----PLAEVEDD-----VEYCGEGGALPTSQHSAGV 921
Db 995 VSVPIAEGESDLDLEDGGEQAQSQFQEVIPKGOEQLOQVERCD--HLTPRSPGCT 1052
Qy 922 QAGDLPETKOLTSDDQGVEMEVSEEDLHLISQSPRKKSDAVASMLSECTIDLND--- 978
Db 1053 SSEDLAPSLG-----ETWKDESVP--QAPAEVDDTSS--SEGSTVDCDLPEE 1096
Qy 979 IFRNLQKTVSPKQDRCPFKGLSCHFLCHTKDRKSPWLWNTRKTCYQIVKISWFES 1038
Db 1097 ILRKLPELADLEEDDDCTEGCIHPCCKLDTTKSPWDVQWQVRKTCYRIVEHSWFES 1156
Qy 1039 FIIFVILLSSGALIPEDVNLSPPOVERKLLRCTDNIFIFILLEMILKWAFAFGPRRYFTS 1098
Db 1157 FIIFMILLSSGLAFEDYDLOKPTVKALLEYTRVFFIFVFEMLLKWAFAFGKYYFTN 1216
Qy 1099 AWCWLDLIVVVSLSL-----MNLPSLSKSFRLRALRPLALSQFEGMKVYVALIS 1151
Db 1217 AWCWLDLIVVVSLSL-----MNLPSLSKSFRLRALRPLALSQFEGMKVYVALIS 1151
Qy 1152 ALPAILNVLVCLIFWVFCILGVNLFSGKFGRCINGDINWYLDFTVFP-----NRSQC 1206
Db 1277 ALPSIMNVLLVCLIFWVLFSGVNLFAKGFWRNCINYTD-----GEFSLVPLSVNNKSDC 1332
Qy 1207 NISN----YSWKVPOVNDVNGVYALLQVATYKGLWEIMNAVDSREKDEQDFEANL 1262
Db 1333 KIONSTGFFWVNVKYNFNDVAMGYLALLQVATYKGLWEIMNAVDSREVNQPKWEDNV 1392
Qy 1263 YAYLVVVFIFGSPFTLNLFIGVIIDNFNQOKKLGQODIFMTBEQKYYNAMKKGTK 1322
Db 1393 YWYLVVVFIFGSPFTLNLFIGVIIDNFNQOKKLGQODIFMTBEQKYYNAMKKGSK 1452
Qy 1323 KPQKPIRPLNKCQAFVDLYTSQVFDVILGLVILNMIIMAESADQPKDKVKTFDILN 1382
Db 1453 KPQKPIRPLNKCQAFVDLYTSQVFDVILGLVILNMIIMAESADQPKDKVKTFDILN 1382
Qy 1383 IAFVVFIECLIKVFLARQHYFTNGWNLFCVGVVLSLSITFLVSR--LEDSISFPPTLF 1441
Db 1513 QFFVAVFTGECVMKMFALRQYFTNGWNVDFIVVLSIASLISAILKLSQSFSPFLF 1572
Qy 1442 RVRLARIGRILRLVRAARGIRTLFLFALMSLPSLNFNTGLLLFLVMFYIATFGMSWFSKV 1501
Db 1573 RVRLARIGRILRLVRAARGIRTLFLFALMSLPSLNFNTGLLLFLVMFYIATFGMSWFSKV 1501

1502 KKGSGIDDFINFETFTGSMCLQFQITTSAGWDTLLNPMLE-AKEHC-----NSSODSC 1554
Db 1633 RWEAGIDDMFNFOITFANSMCLQFQITTSAGWDTLLNPMLE-AKEHC-----NSSODSC 1692
Qy 1555 QOQPAIVYVYSYIIISFLIVVMYIAVILENFATATESESDPLGEDDFEIEFYEWKRPD 1614
Db 1693 GSPAGVGIIFTYIIISFLIVVMYIAVILENFATATESESDPLGEDDFEIEFYEWKRPD 1752
Qy 1615 PSASOFIOYSALSDFADALPEPLRVAKPNKFQFLVMDLPMWMDRLHMDVLFAPFTTVL 1674
Db 1753 PEATOFITFSALSDFADTLGSLRIPKPNRNLIQMDLPLVPGDKIHCLDILFAFTKNVL 1812
Qy 1675 GDSSGLDPMKTMEEKFMEANPEFKLYPIVTTTKKEEEOCAAVIQARYKHM 1728
Db 1813 GESGELDSLKANNEEKFMATNLSKSYEPIATTLRWKQEDISATVIQAIRSYV 1866

RESULT 9

P70276 PRELIMINARY; PRT: 1958 AA.
ID P70276
AC P70276:
DT 01-FEB-1997 (Tremblrel. 02, Created)
ET 01-FEB-1997 (Tremblrel. 02, Last sequence update)
PT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
IE SODIUM CHANNEL, TYPE X, ALPHA POLYPEPTIDE (VOLTAGE-GATED SODIUM CHANNEL).
DE SCN10A OR SNS.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
KW [1]
RP SEQUENCE FROM N.A.
FC STRAIN=129/SV;
XX MEDLINE=97288517; PubMed=9143495;
XA Souslova V., Fox M., Wood J.N., Akopian A.N.;
RT "Cloning and characterization of a mouse sensory neuron tetrodotoxin-
resistant voltage-gated sodium channel gene, Scn10a";
KL Genomics 41:201-209(1997).
LR EMBL; Y09108; CAA70325.1; -;
DR MGD; MGI:108029; Scn10a.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR002111; Cat_channel_trpl.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
KW Ionic channel.
KW SEQUENCE 1958 AA; 220402 MW; AE3811C17721EB72 CRC64;

Query Match 49.7%; Score 4555; DB 11; Length 1958;
Best Local Similarity 50.4%; Pred. No. 0;
Matches 956; Conservative 273; Mismatches 444; Indels 224; Gaps 34;

Qy 15 NFRPFTSLAAIKRIATQIKERKKSKDKAAAE----PQPRQLDKASRKLPLKYGDIP 70
Db 12 NFRFTPSLAEIEKQIAAHRAAKKGRTKQKQKDKSEKPRQLDKACNLPRFYGELP 71
Qy 71 PELVTKPLEDDPYKDKHKTFWLKNKRTIYRFSKRALFILGPNPNRLSRMIRSVHSV 130
Db 72 AELVGEPLDPPYSTHRTFTILLNKRTISRFSATWALWLFSPENLIRRTAIVKSVHSW 131
Qy 131 FSMFTICTVIINCMEFMANSMERSFNDIP---EYFVIGIYILEAVIKILARGFVDESF 187
Db 132 FSIFITVILNVCVMTRT-----DLPEKLEYVTVVYTFEALIKILARGFCLNEFTY 184
Qy 188 LRDPNNWLDVIGTATATCFPGSQVNL---SALRFRVFRALKAISVISGLKIVGALL 244
Db 185 LRDPNNWLDVSIITLA-----YVGAADVLRGISGLRFRVLRALKTVSIPGLKIVGALI 240

Qy	245	RSVKKLVDVMVLTFLCLSTIFALVGOOLFMGILINOKCIKHNCGPNPAS-----KDCFEK	298
Db	241	HSYRKLDADVLTITVFCLSYFALVGLQFKGNLKNCKIKNGTDPKHADNLSLSEMAEDIFIK	300
Qy	299	EKUSEDFIMCGTILWGSRPCPGSTCKDTLTLPDNNYTKFDNFGSFLAFRVMTODSWER	358
Db	301	-PGTTPLLCGNGSDAGHCNPGYVCOKTPDNPDPNTYTFDSFANAFUSLFLKMTQDSWER	359
Qy	359	LYRQILRTSIGYVFVFVVVIFLGSFYLLNLTLAVVTWAYEEQNRRNVAEETAEKRMFOE	418
Db	360	LYQOTLRASGKMYWFFVLVIFLGSFYLVNLILAVVTWAYEEQOATIAETAEKRFQOE	419
Qy	419	AQOLLBREKALVAMGIDRSSL-----NSLQAS	446
Db	420	ALEVLOKEQVLAALGIDTTSFYSHSGSPASKNANERRPVKSRVSEGSTDDNRSPQSD	479
Qy	447	SFSPKRRKFFG-----SKTRKSFPMRG	468
Db	480	PYNQRMSFLGLSGRRRASHGSVPHFRAPSDOVSPDGLIDDGVGHGQDSRRNSILDG	539
Qy	469	SKTAQAS-ASDSEDDASKNP-----QLLEBOTKRLSQNLSP----VDLDFEH-----	508
Db	540	RGACQAGPLPRSPQSPNPGRRKHGEGQLGMPTEGELAAAGTPEGPALDAAGOKNFLSAGY	599
Qy	509	-VDPLHRQRALSAVSILTTITIOEQEFQEPCCPKCNKLASKYLWVDCSPQWLCTIKKVLRT	567
Db	600	LNBPFFRAQRAMSVSMTSVIBELGESKLCPPCLISFAQYLIWECCPKWRKEKMYLLE	659
Qy	568	IMTDPTELAITTCIINTVFYLAVERHHNDDNLKTLIKIGNWFTGFIABMCLKIITALD	627
Db	660	LVTDPPEALTITLCIVNVIVEMAEHYPMTDAFDAMLAQAGNIVFTVPTMEMAEKFIATFD	719
Qy	628	PYHYFRHGMNVFOSIVALLSLADVLNTLUSDNNRSLASLRLRVFKLAKSWPTLNTLIK	687
Db	720	PYTYFQKKMNFIDCVITVTSLLLE--SASKGSGLSVLSRLLRLRVFKLAKSWPTLNMLIK	777
Qy	688	IIGHSVGLNGLNVLTIVTVFISVVGMRFLGCTKE--NKTAYATQERPRRHHMDNFVHS	745
Db	778	IIGNSVGLNGLNTFILAIIVFIPALVGKOLLSENCGRRDGVSVWVNGEKLRRHWCDFHFS	837
Qy	746	FLVVFRILCGEWIENMGCMQMDGSPGICIVFVILIMVIGKLVNLNLFIALLLNSFSNE-	804
Db	838	FLVVFRILCGEWIENMWCM-EVSONYICLTFLTVMLVGNLVNLNLFIALLLNSFSADN	896
Qy	805	-----EKDGSLEGETRTKVQLALDRERRAFSPMLHALOSFCCKKCRK-----	848
Db	897	LTAPEDDGEV-----NNQLALARTQVLIGHRASRAITSYIRSHCFRFPKRPVETQLGMKP	950
Qy	849	-----NSPKRETTESPAG--ENKDSILPDARPWKEYDTDMALYTGOAG	890
Db	951	PLTSCVENHIATDVAAVGNLTLPALSGPENHGDFITDPNVW-----VS	997
Qy	891	APLA-----PLAEVEDDVEYC-----GEGALPTSQHSAGVQAGDLPPETKOLTS	935
Db	998	VPIAEGESDLDELEDVEQASOSSWOESPCKQOELLPOVKOCENHQOARSP--TSGWSS	1055
Qy	936	PDOGVEMEVFSEDLHLSTQSPRRKSDAVMSLSECSITDLND---IFRNLOKVTSPPKQ	992
Db	1056	EDLAPYLGERKWRKRD---NPQVPAEGVDDTSS--SEGSTVDCPDPEILURKLTPELAELDE	1111
Qy	993	PDRCFPKGLSCHFLCHKTOKRSPWMLWNIRKTCYQVHKHSWFSPSFIIFVILLSSGALI	1052
Db	1112	PDDCFTBGCTRCPCCVKVNTSKSPWATGHQVRKTCYRIVEHSWFESFIIFMILLSSGTLA	1171
Qy	1053	FEDVNLSPQOVBEKLLRCDTNIPTFTFLEMLIKWVAFGRFRYFTSAWCWLDLFIVVVSV	1112
Db	1172	FEDVNLBEKPRKRSVLEYTRVFTFTFVPEMLLKWVAFGFKYFTNAMCWLDLFIVNISL	1231
Qy	1113	LSLM-----NLPSLKSPFTLRALRPLRALSQFEGMKVYVALISATIPALNVLLVCLLI	1165
Db	1232	TSIIAKTILEYSOYASIKALURLALRPLRALSRFGRMRVYDALVGALPTSTNNVLLVCLLI	1291

Qy	1166	FWL	VFCILGVNLFSGKFGRCINGTDINWY	-----LDFTEVFNRSOC-----NISNVSWKVPQVN	1219
Qy	1167	Q			
Qy	1168	Q			
Qy	1169	Q			
Qy	1170	Q			
Qy	1171	Q			
Qy	1172	Q			
Qy	1173	Q			
Qy	1174	Q			
Qy	1175	Q			
Qy	1176	Q			
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Qy	1245	Q			
Qy	1246	Q			
Qy	1247	Q			
Qy	1248	Q			</

DR PRINTS: PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1956 AA; 219731 MW; 8FC58EDAD263AC67 CRC64;

Query Match 49.6%; Score 4553; DB 11; Length 1956;
Best Local Similarity 51.1%; Pred. No. 0;
Matches 966; Conservative 269; Mismatches 446; Indels 208; Gaps 36;

QY 15 NFRPPTSLSAAIKKRIAIQERKSKDKAAAE-----PQRPQDLKASRKLKPKLYGDIIP 70
DB 12 NFRPFPESLAEIEKQIAAHAAKAKARTKRGQEDKGKPRQDLKACNOLPKFYGLP 71
QY 71 PELVTKPLEDDPYKYDKHRTMVLNKKRTIYRFSAKRALFILGPNPLRSLMIRISVHSV 130
DB 72 AELVGEPLDDPFYTHRTMVLNKKSTISRFSATWALWLFSPNLIRRTAIVKSVSHV 131
QY 131 FMSFICIVINCMPMANSERSFNDIP---EYVFIGIYLEAVIKILARGFIVDFRSF 187
DB 132 FSIFFITILVNCVMTRT-----DLPEKVEYVFTVIYTFEALIKILARGFCLNEPTY 184
QY 188 LRDPNWLDFIVIGTAIATCPGSOVNL---SALRTFRVFRALKAKAISVISGLKVIIVGALL 244
DB 185 LRDPNWLDFSVITLA---YVGAIDURGIGSLRTFRVLRALKTVSVIPGLKVIIVGALI 240
QY 245 RSVKRLVDVMVLTFLCLSFALVGQOLPMGILNOKIKHNCGPNPASNKDCFEKE----- 299
DB 241 HSVRLADVTILTVECLSVFALVGLQLPKGNLKNKICRNGTDPHKADNLSEMAEYIFIK 300
QY 300 KDSDFIMCGTWLGSRPCNGSTCDKTLNPDNNYTKFDNFGWGFPLAMFRVMTODSWRL 359
DB 301 PGTTDPLLCGNGSDAGHCPGGVCLKTPDNDPNDFNYTSPDSFAWFLSLFRLMTODSWRL 360
QY 360 YRQILRTSGIYVFEFVVVIFLGSFYLLNLFLAVVTWAYEQRNVAETAEAKEMFOEA 419
DB 361 YQOTLRAGKMYMFFVLVIFLGSFYLVNLFLAVVTWAYEQSQATIAEIEAKEKFOEA 420
QY 420 QOLLREEKALVAMGIDRSLNSLQASFSF-----KRRKFGS----- 458
DB 421 LEVLQKEQVLAALGIDTSLQSHSGSPLASKNANRRPRVKSRSVSEGSTDDNRSPOSDP 480
QY 459 --KTRKSFPMGSKTAQAS-----ASDSED----- 481
DB 481 YNQRMSPLGLSSGRRRASHGSVFHFRAPSQDISFPDGIIDDGVFHGDQESRRGSILLGR 540
QY 482 -----DASKNP-----QLLEOTKRLSONLP-----VDLFDEHV----- 509
DB 541 GAGOTGPLRSPLOSPNRRHGEQGLVPTGELTAGAPEGPALDTTGOKSFLSAGYL 600
QY 510 -DPLHRORALSAVILTIIOEQEKFPQPCPGKNLASKYLVWDCSPQWLICIKKVLRTI 568
DB 601 NEPPRAORAMSVVIMTSVIEELESKLKCPCLISFAQKYLIEWECCPKRKKFMAIFEL 660
QY 569 MTDFTTELATIGIITVFLAVHHNMDMLKILKIGNVWVFGIFIAEMLKIIALDP 628
DB 661 VTDPAELTITPLCVNTVFMAMEHYPMTDADFAMLAQAGNIVFTVFTMEMAFKIIAFDP 720
QY 629 YHYPRHGWNVFDSIVALLSLADVLNLTSDNNRSLASRLVRLVEKLAKSWPTLNTLIKI 688
DB 721 YYYQKKNVFDVIVTVLSLEL---SASKGSLSVLFTFRLRLVRLVEKLAKSWPTLNTLIKI 778
QY 689 IGHSVAGALNLTJVVLTITVIFTSVVGMLRFGTKF--NKTAYATQERPRRRWHMDFYHSF 746
DB 779 IGNSVAGALNLTFLAIIIVFIFALVGKQLLSEDYGCRKDGVSVMNGEKLWHMCDFFHSF 838
QY 747 LVVPRILCGEWINWCMQMDGSPCLIVFVLWIGVLVNLFIALLNLSFSNE-- 804
DB 839 LVVPRILCGEWINWCM--EVSOKSICLFLFTVWGLNVLNLFIALNLSFSADNL 897
QY 805 ---EKDGSLEGETKTKVQALDRFRAFSFMLHALQSFCCKKCRKNSPKPKETFE--- 858
DB 898 TAPEDQGEV-----NLQALARIQVLGHRASRAIASYISSHCRFR---WPKVETQLGM 948

QY 859 ---SPAGENKDSILPDA-----RP-----WKYEYTDMDALYTGQACAPLA---- 894
DB 949 KPPLTSSSEAKNHIATDAVSAAGVNLTKFALSPKKNHGDFTIDPNVW---VSVPIAEGS 1005
QY 895 PLAIVEDDVEYC-----GEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQGVEM 943
DB 1006 DLDELEDEMEQASQSSWQEDPKGOEQOLPQVKCENIQAARSP--ASMMSSEDLAPYLG 1063
QY 944 EYFSEEDLHLSTQSPRKSADVMSLSECTIDLND---IFRNLQTVSPKKQPDRCFPKG 1000
DB 1064 ESWRKD---SPQVPAEGVDDTSS--SEGSTVDCPQPEETLRKIPELADLDLDPDCFTBG 1119
QY 1001 LSCFLCHKTOKRKSPPWLWNIRKTCQIVKHSFESFIIIVILLSSCALIFEDVNLPS 1060
DB 1120 CTRRCPCCNVNTSKSPWATGMQVRKATCYRIVEHSFESFIIPMILLSSGALAFEDONYLEE 1179
QY 1061 RPOVEKLLRVTDNIFTFILLEMLKLVAFGFRFRYFTSAWCWLDLFIIVVSVLSLM---- 1116
DB 1180 KPRVKSULEYTDRTVFTFIFVEMLLKWAYGFKYFTNACWLDLFIIVNISLTSIAKIL 1239
QY 1117 ---NLPSLKSFTLRALRPLRALSQFEGMKVVVYALISAIPAILNVLVCLIFWVFCIL 1173
DB 1240 EYSDVASIKALRTLALRPLRALSFEGRVGVVVDALVGAIPSIMNVLLVCLIFWLFISFM 1299
QY 1174 GVNLFSGKFGRCINCTDINMY--LDFTVPMARSQCNISN---YSMKVPOVNFDMVGNAY 1227
DB 1300 GVNLPAGFKSCVD--TRNPFNSNVNSTVMNKNSECHNQNSTGHFFPMVNVKNFDMVANGY 1358
QY 1228 LALLQVATYKGWLEIMNAADVDSREKDEQDFEANYLYAYLYFVVFIFGFSFTLNLFIGVI 1287
DB 1359 LALLQVATFKGMDIMYAAVDSGEINSOPNENNLMYLYFVVFIFGFSFTLNLFIGVI 1418
QY 1288 IDNENQOKKLGQODIFMTEQKKYNNAMKLGTKKKPKQIPRPLUNKCOAFVDFLVTQV 1347
DB 1419 IDNENQOKKLGQODIFMTEQKKYNNAMKLGSKKKPKQIPRPLUNKYQGFVDFIVTRQA 1478
QY 1348 FVITILGLILVNIIMMAESADQPKDKVKTFDILNIAFVVIETIRCLIKVFAALROHYETN 1407
DB 1479 FDIIMWLICLNMTIMVETDEQGEETKVLGRINQFVAVFTGECVMKMFALROYFTN 1538
QY 1408 GWNLFDCVWVVLSTISLTVSR--LEDSISFPPTLFRVVRVLARIGRILRLVRAARGIRTL 1466
DB 1539 GWNVDFEIVVILSIGSLLSAILKSLNLYFSPTLFRVIRLARIGRILRLVRAARGIRTL 1598
QY 1467 FALMKSPLSPENIGLLFLVNFYIAFGMSWFSKVKSGIDIDFNFETFTGSMCLCFQI 1526
DB 1599 FALMKSUPALENIGLLFLVNFYISIFGMASFANVVDAGIDDMFNEXTFGSMCLCFQI 1658
QY 1527 TTSAGWDTLLNPMLE-AKEHC-----NSSQDSQOQPIAVVYFVSIIISFLIVVMY 1579
DB 1659 TTSAGWGLLSPILNTGPPYCDPNLPNSNGRGNGSGSPAVGIIFTTIIISFLIVVMY 1718
QY 1580 IAVILENFNTATESEDPGLGDDFEIFYVWEKEDPEASQFIQYSALSDFADALPELVR 1639
DB 1719 IAVILENFVATESETEPLSDDDFMEYETWEKEDPEATQFIASALSDFADTLGGLRI 1778
QY 1640 AKPNKFLVMDLPMVMDRLHMDVLEAFTRVILGDSGLDTHKTMKEEFMEANPKK 1699
DB 1779 PKPQNIILQMDLPLVPGDKTHCLDILFAFTKNVILGESGELDSLKTNMEEFMATNLSKA 1838
QY 1700 LYEPVITVTKRKEEQAAGAAVIOQRAYRKHM 1728
DB 1839 SYEPIATTLRWKQEDLSATVLOKAYRSM 1867
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Q15858 PRELIMINARY; PRT; 1977 AA.
ID Q15858
AC Q15858:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
SODIUM CHANNEL ALPHA SUBUNIT.

QY 190 DPWNWLDFTVIGTATATCPGQSVNLSALRTRFRVFRALKATSAISGLKVIIVGALLRSVKK 249
Db 186 DPWNWLDFTVIVFAYLITEV- NLGNVSALRTRFRVLRALKTISVIPGLKTIIVGALLQSVKK 244
QY 250 LYDVWVLLTCLSLFALYGOQLFMGLINQKCIKHNGCPNPASNKDCPFKEKD- ----- 301
Db 245 LSDVITLAVFCLSVFALIGLQFMGLHKHKLURKIENETLESINSESEEDYKKFYFYL 304
QY 302 --SEDFIMCGTWLGRPCPGSTCDKTLTNPNNYTKFDNFCWGFSLAMFRVMTQDSWRL 359
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QY 360 YQOILRTSGIYVFFVVFVIFLGSYLLNLTLAVVTMAYEQNRNVAAETAKRMFOBA 419
Db 365 YQOTLRAAGKTYMIFVVVIFLGSYLLNLTLAVVAMAYEQNANIEAKQKELEFQOM 424
QY 420 QQLR--BEKALVA-----MGIDRSLNSLQASSPSFKKRFEGSK----- 459
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QY 460 -----TRKSPFM----- 466
Db 485 KLSGEEKGDDKLSKSESEISRKQFHLGVEGRLAREKLSAPNOSPISIRGSLFSA 544
QY 467 --RGSKTA-----QASASDSEDDAS 484
Db 545 RRSRTSLFSFKGRKDIGSETEFADDEHSIFGDNESRGSFLFPQRPQERRSSNLQAS 604
QY 485 KNPQLLEOTKRL-----SONLPVDLFDEHV----- 509
Db 605 RSPPLMONGKMHSAVDCNGVSVLDGPSALMLPNQLLPEVIIIDKATSDSGTTOIRKK 664
QY 510 -----DPLHRORALSAVSILTIIOEQEFQOEPFCGCKNLASKYLWDCS 555
Db 665 RRSYLLSEDMNDPLHQRAMSASILTNTVEELESQKCPSWYRFAHTFLIWNCS 724
QY 556 POWLCIKKVRITMDPTELATITCIINTVFLAVEHNNDDNLTKILKIGNWVFTGIF 615
Db 725 PWIKFKFIYIIVMDPFDLAIITICIVNLFMAHEHPMTEEFKNVLVGVNLVFTGIF 784
QY 616 IAEMLCKIADPYHYFRHGNVFDISVALLSLADLVNTLSD--NNRSFLASRLVRFK 674
Db 785 AEAMVYKLTAMPDEYFQGVNVDLSLTVLSLSELF--LADVEGLSVLRSLRVRFK 841
QY 675 LAKSWPTLNTLKIIGHSGVAGLNLTVLTIWVFTSVVGMRLFTGKKN--TAYATQERP 733
Db 842 LAKSWPTLNTLKIIGNSGVPLGNLTLLAIIVFIFAVVGMQLFGKSKYCKECVCKINDDCS 901
QY 734 RRRHMDNFYHSLVFRILCEWIENTMWGCMODMGDGPLCIIVFVLIWVIGKLVVNL 793
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Db 1058 GFGSSMDKYLMEESDQSHFNPSL-----IVTVPIAGESDLENMNTTEELSSDSESEYS 1112
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Db 1173 KIWNIRKTCYRIVHSFESFLIFVILLSSGALLFEDVNIIEKKTKIKIILEYADKIETY 1232
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QY 1191 INMYLDFTEVNRSOC-----NISVSKKPOVNDNVGNAYLALLOVATYKGLIEMA 1245
Db 1353 DSRF--PTQVSKRSECFALMNGSQNRWKNLKVNDNGLRYSLLQVATFGWMDIMYA 1411
QY 1246 AVDSREKDEQDPFEANLAYLVVYVFIIFGSEFTNLNLFITGVIIIDNFNOQKLLGGODIFM 1305
Db 1412 AVDSVNVDOQPSYEHNLWYIYFVIFIFGSEFTNLNLFITGVIIIDNFNOQKLLGGODIFM 1471
QY 1306 TEEQKYYNAMKKGTKKPKQPIRPLNKCQAFVEDLVTSQFVDVILGLIVNLMIEMA 1365
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QY 1366 ESADQPKOVKKTFDILNIAFVVIETIECLIKVFALRQHYFTNGWNLFCVWVLSIISTL 1425
Db 1532 EKEGSDYNTDVLVYNVVFIIILFTGECVLKLSURHYFTTIGNNIFDFVWVLSIVGMF 1591
QY 1426 VSRLESDSITSPPTLFRVVRRLARIGRILRLVRAARGIRTLLEFALMMSLPSLFNIGLILFL 1485
Db 1592 LAELIET--YFVSPTLFRVIRLARIGRILRLKAGAKIRTLLEFALMMSLPALENIGLILFL 1650
QY 1486 VMFIYALFGMSWFSKVGKSGIDDIINFETFTGSMCLCPOITTSAGWDTLLNPMLEA--- 1542
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QY 1598 LCEDDFEIYEWWEKFDPEASQIOYSAISDFADALPEPLRVAKPNKFOFLVMDLPMVNG 1657
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QY 1658 DRHCLMDVLFAFTTRVLGSSGLDTMTKMTMEKFMANPFKKLYEPVITVTKRKEEEOGA 1717
Db 1831 DRHCLMDILFAFTTRVLGSEGMDSLRSQMEERFNSANPSKVSYPEITVTKRKEEEDVSA 1890
QY 1718 AVIQRAYKHKMEKMWKRLKDRSSSS 1743
Db 1891 TVIQRAYRRY-----RLRONVKNISS 1911

Search completed: February 27, 2002, 01:38:16
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 22:39:07 ; Search time 8647.11 Seconds
(without alignments)
570.440 Million cell updates/sec

Title: US-09-646-224A-3
Perfect score: 299
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Scoring table: IDENTITY NUC
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Searched: 1472140 seqs, 8248589755 residues
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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31: em_htgo_inv.*
32: em_htgo_rod.*
33: em_htg_hum.*
34: em_htg_inv.*
35: em_htg_rod.*
36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
1	299	100.0	299	6	AX017219	AX017219 Sequence
2	276.4	92.4	5728	9	AF150882	AF150882 Homo sapi
3	276.4	92.4	6528	9	AF109737	AF109737 Homo sapi
4	204.4	68.4	6237	9	AF188679	AF188679 Homo sapi
5	167.8	56.1	5908	6	E36122	E36122 Nucleic aci
6	160.4	53.6	5334	6	E36125	E36125 Nucleic aci
7	160	53.5	5905	10	AF059030	AF059030 Rattus no
8	159.2	53.2	5858	10	AF118044	AF118044 Mus muscu
9	159.2	53.2	5891	10	AB031389	AB031389 Mus muscu
10	158.4	53.0	5897	6	AX017217	AX017217 Sequence
11	151	50.5	5849	10	RNO237852	AF1237852 Rattus no
12	45.8	15.3	5874	9	AF117907	AF117907 Homo sapi
13	44.2	14.8	6726	4	CFU60590	U60590 Canis famli
14	38.6	12.9	128398	9	AC004817	AC004817 Homo sapi
15	38.4	12.8	6527	6	A58859	A58859 Sequence 7
16	38.4	12.8	7052	6	A58857	A58857 Sequence 5
17	37.8	12.6	6344	10	RNO53833	U53833 Rattus norv
18	37.6	12.6	167372	9	AC004945	AC004945 Homo sapi
19	36.8	12.3	6524	6	A58853	A58853 Sequence 1
20	36.8	12.3	6524	10	RNSNS	X52184 R.norvegicu
21	36.6	12.2	149490	2	AL589885	AL589885 Homo sapi
22	36.2	12.1	182443	2	AC009451	AC009451 Homo sapi
23	36.2	12.1	199534	2	AC025959	AC025959 Homo sapi
24	36	12.0	116106	9	AL136080	AL136080 Human DNA
25	36	12.0	145105	2	AC018432	AC018432 Homo sapi
26	36	12.0	172052	9	AL157769	AL157769 Human DNA
27	35.8	12.0	180519	2	AC024931	AC024931 Homo sapi
28	35.8	12.0	187520	2	AF282854	AF282854 Homo sapi
29	35.6	11.9	6096	3	BGU73583	U73583 Blattella g
30	35.6	11.9	6096	3	BGU73584	U73584 Blattella g
31	35.6	11.9	129473	2	AC040158	AC040158 Homo sapi
32	35.6	11.9	143900	2	AC092137	AC092137 Homo sapi
33	35.4	11.8	39854	9	AC020954	AC020954 Homo sapi
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36	35.4	11.8	157921	2	AC027726	AC027726 Homo sapi
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38	34.8	11.6	6373	10	MMSNS	Y09108 M.musculus
39	34.6	11.6	205195	2	AC025963	AC025963 Homo sapi
40	34.4	11.5	163067	2	AC022959	AC022959 Homo sapi
41	34.4	11.5	211357	2	AC021136	AC021136 Homo sapi
42	34.2	11.4	6822	10	RNSCIII	Y00766 Rat mRNA fo
43	34.2	11.4	141534	9	CNS01DS0	AL121503 Human chr
44	34.2	11.4	186118	2	AC016973	AC016973 Homo sapi
45	33.8	11.3	68692	9	HSDJ468N4	AL121752 Human DNA

ALIGNMENTS

RESULT 1

AX017219
LOCUS AX017219 299 bp DNA
DEFINITION Sequence 3 from Patent WO9947670.
ACCESSION AX017219 PAT 07-SEP-2000
VERSION AX017219.1 GI:10042139
KEYWORDS human.
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;
REFERENCE 1 (bases 1 to 299)
AUTHORS Tate,S.N., Grose,D.T. and Hick,C.A.
TITLE Mammalian sodium channel proteins
JOURNAL Patent: WO 9947670-A 3 23-SEP-1999;
TATE SIMON NICHOLAS (GB); GLAXO GROUP LTD (GB); GROSE DAVID THOMAS (GB); HICK CAROLINE ANNE (GB)
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300 AAAAGGAGAAAAAGAGTCTAAAGACGACAGAGGAAGTACCCAGCTTCGGCCCTCAGC 297
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241 ttgacctaagggcctcaggaagtgtgccaa-cctcatggcgacaaatcctcggagct 297
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360 TTGACCTAAGGCTCAGGAAGTTCGCCAAGCTCTATGCGACATTCCTCTGTCGAGCT 417
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RESULT 4
AF188679
LOCUS
DEFINITION Homo sapiens voltage-gated sodium channel type XI alpha subunit
(SCN11A) mRNA, complete cds.
ACCESSION AF188679
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6237)
AUTHORS Dib-Hajj, S.D., Tyrell, L., Cummins, T.R., Black, J.A., Wood, P.M. &
Waxman, S.G.
TITLE Two tetrodotoxin-resistant sodium channels in human dorsal root
ganglion neurons
JOURNAL FEBS Lett. 462 (1-2), 117-120 (1999)
MEDLINE 20047838
REFERENCE 2 (bases 1 to 6237)
AUTHORS Dib-Hajj, S.D., Tyrell, L., Cummins, T.R., Black, J.A. and Waxman,
S.G.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A,
Bldg. 34, 950 Campbell Ave., West Haven, CT 06516, USA
FEATURES
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/db_xref="taxon:9606"
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/tissue_type="dorsal root ganglia"
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/translation="MDRCYPIVFPDERPPTSDSLAAIEKRIAIOKEKKK
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EPHLTIQDPRKKSVDVTSILSECTIDLQDGWLPPEWPKKQPERCLPKFGG
SVDRKPPVYIWNLRKTCFLQVKNHSFESFTIFVILLSSGALIFEDVHLN
LUNCTDITFIIFHILEMWLIKWAFGFKYFTSACWCDFTIIVTSVTTLNLA
RTIALRLPDLASQFEGMKVNNVNALIGAIPAILNVLAVCLIFWLVCPLGILVY
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IYAAVSTEREQOPEFBSNSLGIYFVVFIIIFGSFFTLNLFIVGIIIDFNNOOKKLG
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BASE COUNT 1761 a 1370 c 1366 g 1740 t
ORIGIN

Query Match 68.4%; Score 204.4; DB 9; Length 6237;
Best Local Similarity 96.9%; Pred. No. 5.4e-52;
Matches 219; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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Db 23 GGGTGAAGATGGATGACAGATGCTACCCAGCAATCTTTCCAGATGAGCGGAATTTCCGCC 82
QY 133 ccttcactccgactctctgctgcaattgagaagcgatgcatccataaagagagaaa 192
Db 83 CCTTCACCTCCGACTCTCTGCTGCAATGAGAGCGGATGCTCCATCCAAAGAGAGAAA 142
QY 193 agaagctaaagacagacagagagaagtacccccagcctcaacctcagcttgacctaaagg 252
Db 143 AGAGCTCTAAAGACACAGACAGAGAGTACCCAGCCTCGCGCTTGACCTTAAAGG 202
QY 253 cctccagaagttgcccaa-ctctatggcgacaatcctcgaggct 297
Db 203 CCTCCAGGAGTTGCCAAGCTCTATGGCGACATTTCTCGTGAGCT 248

RESULT 5
E36122
LOCUS E36122 5908 bp DNA PAT 07-FEB-2001
DEFINITION Nucleic acid encoding sodium channel of nerve tissue.
ACCESSION E36122
VERSION E36122.1 GI:13022505
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus.
REFERENCE 1 (bases 1 to 5908)
AUTHORS Paul,S.D.L.L., Fish,R.K.D.D., Rambert and Laksmi,S.
TITLE Nucleic acid encoding sodium channel of nerve tissue
JOURNAL Patent: JP 1999235186-A 1 31-AUG-1999;
F HOFFMANN LA ROCHE AG
COMMENT OS Rattus sp. (rat)
PN JP 1999235186-A/1
PD 31-AUG-1999
PF 20-NOV-1998 JP 1998331769
PR 20-NOV-1997 US 60/066225
PI PAUL SHATUA DAITORICHI,LINDA MARIE FISH,RINA KEIRU, PI
DOUGLAS KENESU RAMBERT,
LAKSMI SANGEIMUSUWARAN
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12N15/02,C12P21/02, PC
C12P21/08,
PC C12Q1/68,G01N33/53,G01N33/577,G01N33/68//C12N5/10,C12R1:91),
PC (C12P21/02,C12R1:91), (C12P21/08,C12R1:91),C12N15/00,C12N5/00,
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PC (C12N5/00,C12R1:91)
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BASE COUNT 1458 a 1474 c 1451 g 1525 t
ORIGIN

Query Match 56.1%; Score 167.8; DB 6; Length 5908;
Best Local Similarity 82.6%; Pred. No. 9.7e-41;
Matches 204; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
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Db 51 GTGTCTTCTGCCCTCCTCAGGGTGAAGATGAGGAGAGGACTACCCGGTGATCTTCCC 110
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QY 292 gaggctt 298
Db 291 TGAGCTT 297

RESULT 6
E36125
LOCUS E36125 5334 bp DNA PAT 07-FEB-2001
DEFINITION Nucleic acid encoding sodium channel of nerve tissue.
ACCESSION E36125
VERSION E36125.1 GI:13022508
KEYWORDS JP 1999235186-A/4.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 5334)
AUTHORS Paul,S.D.L.L., Fish,R.K.D.D., Rambert and Laksmi,S.
TITLE Nucleic acid encoding sodium channel of nerve tissue
JOURNAL Patent: JP 1999235186-A 4 31-AUG-1999;
F HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 1999235186-A/4
PD 31-AUG-1999
PF 20-NOV-1998 JP 1998331769
PR 20-NOV-1997 US 60/066225
PI PAUL SHATUA DAITORICHI,LINDA MARIE FISH,RINA KEIRU, PI
DOUGLAS KENESU RAMBERT,
LAKSMI SANGEIMUSUWARAN
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12N15/02,C12P21/02, PC
C12P21/08,
PC C12Q1/68,G01N33/53,G01N33/577,G01N33/68//C12N5/10,C12R1:91),
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RESULT 7
AF059030
LOCUS AF059030 5905 bp mRNA ROD 16-JUL-2001
DEFINITION Rattus norvegicus voltage-gated Na channel alpha subunit Nan mRNA, complete cds.
ACCESSION AF059030
VERSION AF059030.2 GI:14719821
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 5905)
AUTHORS Dib-Hajj,S.D., Tyrrell,L., Black,J.A. and Waxman,S.G.
TITLE Nan, a novel voltage-gated Na channel, is expressed preferentially in peripheral sensory neurons and down-regulated after axotomy
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8963-8968 (1998)
MEDLINE 98338024
REFERENCE 2 (bases 1 to 5905)
AUTHORS Dib-Hajj,S.D., Tyrrell,L., Black,J.A. and Waxman,S.G.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1998) Neurology, Yale University Medical School, 333 Cedar St., New Haven, CT 06510, USA
COMMENT On Jul 16, 2001 this sequence version replaced gi:3372614.
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Best Local Similarity 84.2%; Pred. No. 2.4e-38;
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Dbb 223 GCCTCCAGGAAGTTACCTAAGCTTTATGTTGACATTCCTCCCTGAGCTT 270

RESULT 8
AF118044
LOCUS AF118044 5858 bp mRNA ROD 07-SEP-1999
DEFINITION Mus musculus voltage-gated sodium channel Nan (Scnlla) mRNA, complete cds.
ACCESSION AF118044
VERSION AF118044.1 GI:5833119
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5858)
AUTHORS Dib-Hajj,S.D., Tyrrell,L., Escayg,A., Wood,P.M., Meisler,M.H. and Waxman,S.G.
TITLE Coding sequence, genomic organization, and conserved chromosomal localization of the mouse gene Scnlla encoding the sodium channel Nan
JOURNAL Genomics 59 (3), 309-318 (1999)
MEDLINE 99375324
PUBMED 10444332
REFERENCE 2 (bases 1 to 5858)
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AUTHORS
TITLE
JOURNAL

Dib-Hajj, S.D., Tyrell, L. and Waxman, S.G.
Direct Submission
Submitted (05-JAN-1999) Neuroscience Research Center, 127A, Yale
University/VAMC, 950 Campbell Ave, West Haven, Ct 06516, USA

FEATURES

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Location/Qualifiers

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DEFINITION

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ACCESSION

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AB031389.1

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ORGANISM

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AF117907 5874 bp mRNA PRI 18-MAY-1999
LOCUS Homo sapiens tetrodotoxin-resistant voltage-gated sodium channel
DEFINITION (SCN10A) mRNA, complete cds.
ACCESSION AF117907
VERSION AF117907.1 GI:4838144
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
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VATESTEPELSEDDFDMFYETWEKDFPEATQIFTSALSDFADLSGLRPLRPNRNI
LIQMDLPLVFGDKITHCLDILFAETKNVIGSEGLDSLKANMEKFMATNLSKSYEPI
ATTLLRWQEDISATVIOKAYRSVYTRGLSMDLNSALNTPCPVRAEEAASDEGFAFTAN
ENCVLDPKSETASATFPSPSYVTRGLSDRVNMRMTSSSIQNEDEATSMELIAPCP"
BASE COUNT 1434 a 1552 c 1428 g 1460 t
ORIGIN
Query Match 15.3%; Score 45.8; DB 9; Length 5874;
Best Local Similarity 60.7%; Pred. No. 0.0031;
Matches 99; Conservative 0; Mismatches 52; Indels 12; Gaps 1;
```


Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_DA0091H08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Author's contribution:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 14 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/FTP/CHR14>, send <mailto:green@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-6, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics, 6:84-9 (1994). The library is from one female donor. For further details, see <http://bacpac.med.buffalo.edu/>. The clone is available from Genome Systems, Inc. (<http://www.genomesystems.com>).

VECTOR: pPAC4

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP1-261b10; the clone sequenced to the right is RP5-11631l1, 200 bp overlap. Actual start of this clone is at base position 1 of RP6-91lH8; actual end is at base position 128202 of RP6-91lH8.

FEATURES

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	/map="14q24.3"	repeat_region	17139. .17219
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 22:49:44 ; Search time 478.33 Seconds
(without alignments)
535.907 Million cell updates/sec

Title: US-09-646-224A-3

Perfect score: 299

Sequence: 1 atctaggcaggtgtttt.....cgacaatctcggaggctttt 299

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	299	100.0	299	AAZ21481	Human sensory neur
2	204.4	68.4	5860	AAF30101	Human sodium chann
3	167.8	56.1	5908	AA560241	CDNA encoding type
4	160.4	53.6	5334	AA560244	Stabilised cDNA en
5	160	53.5	5875	AA560244	Rat sodium channel
6	160	53.5	5875	AA560244	Rat sodium channel
7	158.4	53.0	5897	AA221480	Rat sensory neuron
8	157.8	52.8	5822	AA560241	Mouse sodium chann
9	157.8	52.8	5822	AA560241	Mouse sodium chann
10	45.8	15.3	5874	AA560241	Human hPN3 CDNA se
11	44.2	14.8	6606	AA560872	NaNG polypeptide e

12	38.4	12.8	6527	18	AA777806
13	38.4	12.8	7052	18	AA777805
14	37.8	12.6	6344	22	AAF57009
15	36.8	12.3	6524	18	AA777803
16	34.6	11.6	6729	20	AA12974
17	33	11.0	7608	16	AA074118
18	32.8	11.0	1458	22	AA50931
19	32.8	11.0	1593	22	AA50930
20	32.4	10.8	1932	22	AA03528
21	31.6	10.6	3219	21	AA295276
22	31.6	10.6	8378	22	AA55763
23	31.6	10.6	8378	22	AA55764
24	31.4	10.5	483	22	AA55766
25	31	10.4	855	19	AA52378
26	31	10.4	13425	19	AA52284
27	30.4	10.2	481	20	AA06952
28	30.4	10.2	1951	22	AA52291
29	30.4	10.2	3442	22	AA52313
30	30.4	10.2	6513	17	AA52338
31	30.4	10.2	6513	17	AA52338
32	30.4	10.2	6519	20	AA52500
33	30.2	10.1	1025	22	AA55828
34	30.2	10.1	1066	19	AA53410
35	30.2	10.1	9112	22	AA55823
36	30.2	10.1	9112	22	AA55824
37	29.8	10.0	558	22	AA510196
38	29.8	10.0	4054	20	AA513188
39	29.6	9.9	531	21	AA569707
40	29.6	9.9	2142	22	AA515254
41	29.6	9.9	2198	22	AA514344
42	29.6	9.9	2392	20	AA561221
43	29.4	9.8	3834	22	AA501281
44	29	9.7	1074	20	AA200427
45	29	9.7	1297	22	AA502555

ALIGNMENTS

RESULT 1

AAZ21481
ID AAZ21481 standard; cDNA; 299 BP.

AC AAZ21481;

DT 03-DEC-1999 (first entry)

XX Human sensory neurone specific 2a nucleotide sequence fragment #1.

XX Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss.

XX Homo sapiens.

XX WO9947670-A1.

XX 23-SEP-1999.

XX 18-MAR-1999; 99WO-GB00838.

XX 18-MAR-1998; 98GB-0005793.

XX (GLAX) GLAXO GROUP LTD.

XX Grose DT, Hick CA, Tate SN;

XX WPI; 1999-562112/47.

XX Mammalian sodium channel protein for treating pain and hypersensitivity

XX Claim 6; Page 66; 73pp; English.

XX AAZ21481 to AAZ21495 represent fragments of the human sensory neurone

XX

CC specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel
 CC protein. SNS-2a can be used in a method for the identification of a
 CC modulator of a sodium channel, and for assaying for compounds which
 CC modulate sodium flux. The sodium channel modulators can be used in a
 CC medicament for the treatment of pain or hypersensitivity.

XX
 SQ Sequence 299 BP; 74 A; 81 C; 73 G; 71 T; 0 other;

Query Match 100.0%; Score 299; DB 20; Length 299;
 Best Local Similarity 100.0%; Pred. No. 4.4e-87;
 Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atcttaggcaggctgtttattccgcctctctgagcgttcttgaggtatctgtggttg 60
 Db 1 atcttaggcaggctgtttattccgcctctctgagcgttcttgaggtatctgtggttg 60
 Qy 61 tctctgtctgaggtgagatgacagatgacatccagtaattcttccagatgagc 120
 Db 61 tctctgtctgaggtgagatgacagatgacatccagtaattcttccagatgagc 120
 Qy 121 ggaattccgcctctccactctccactctctggtgcaatgagaagcggattgccatcc 180
 Db 121 ggaattccgcctctccactctccactctctggtgcaatgagaagcggattgccatcc 180
 Qy 181 aaaaggagaaaaaagaagtctaaagaccagacagaggaagtaacccagctcaacctcagc 240
 Db 181 aaaaggagaaaaaagaagtctaaagaccagacagaggaagtaacccagctcaacctcagc 240
 Qy 241 ttgacctaaaggctccagggaagtggcccaactctatggcgacaatctcggaggcttt 299
 Db 241 ttgacctaaaggctccagggaagtggcccaactctatggcgacaatctcggaggcttt 299

RESULT 2

AAF30101
 ID AAF30101 standard; cDNA; 5860 BP.

XX
 AC AAF30101;

XX
 DT 30-APR-2001 (first entry)

XX
 XX Human sodium channel NaN cDNA.

XX
 KW Sodium channel; NaN; human; tetrodotoxin resistant; pain;
 KW paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
 KW diagnosis; ss.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT CDS 31..5402
 FT /*tag= a

XX
 PN WO200105831-A1.

XX
 PD 25-JAN-2001.

XX
 PF 14-JUL-2000; 2000WO-US19342.

XX
 PR 16-JUL-1999; 99US-0354147.

XX
 PA (UYIA) UNIV YALE.

XX
 FI Dib-Hajj S, Waxman SG;

XX
 DR WPI; 2001-103147/11.

XX
 DR P-PSDB; AAB20121.

XX
 PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium
 PT channels, useful for preventing, diagnosing and treating pain,
 PT paraesthesia and/or hyperexcitability phenomena -

XX

PS Claim 1; Fig 11A; 162pp; English.

XX The present sequence is that of cDNA encoding a novel human
 CC tetrodotoxin resistant sodium channel, termed NaN (see AAB20121).
 CC The cDNA was isolated from a human dorsal root ganglia tissue cDNA
 CC library by PCR amplification (see also AAF30122-23). NaN belongs
 CC to the a-subunit voltage-gated sodium channel protein family and
 CC produces a TTX-R sodium current. Such channels underlie the
 CC generation and propagation of impulses in excitable cells such as
 CC neurons and muscle fibres. Preferential expression of NaN on
 CC sensory neurons innervating the body (dorsal root ganglia) and the
 CC face (trigeminal ganglia), but not on other neurons, makes it a
 CC very useful target for diagnostic and/or therapeutic uses in
 CC relation to acute and/or chronic pain pathologies. A claimed
 CC method of treating pain, paraesthesia and/or hyperexcitability
 CC phenomena in a human or animal subject involves administering an
 CC agent that alters sodium current flow through NaN channels, or
 CC which modulates transcription or translation of NaN mRNA, in
 CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids
 CC are used in gene therapy to correct disorders associated with
 CC decreased sodium channel expression or (antisense) to down-regulate
 CC NaN expression, in the diagnosis of disease, and in the recombinant
 CC production of NaN polypeptides.

XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 other;

Query Match 68.4%; Score 204.4; DB 22; Length 5860;
 Best Local Similarity 96.9%; Pred. No. 6.5e-56;
 Matches 219; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 73 ggggtgaagatggatgacagatgctaccagtaattcttccagatgagcggaattccgcc 132
 Db 73 ggggtgaagatggatgacagatgctaccagtaattcttccagatgagcggaattccgcc 82
 Qy 133 ccttcactccgactctctgctgcaattgagaagcggatgctccatccaaaggagaaaa 192
 Db 133 ccttcactccgactctctgctgcaattgagaagcggatgctccatccaaaggagaaaa 142
 Qy 193 agaagctaaagaccagacagaggaagtacccacgctccacccagcttgacctaaagg 252
 Db 143 agaagctaaagaccagacagaggaagtacccacgctccacccagcttgacctaaagg 202
 Qy 253 cctccaggaagttgcccaa-ctctatggcgacaatctcggaggct 297
 Db 203 cctccaggaagttgcccaaagctctatggcgacaatctcctcgtgagct 248

RESULT 3

AAX60241

ID AAX60241 standard; cDNA; 5908 BP.

XX
 AC AAX60241;

XX
 DT 11-AUG-1999 (first entry)

XX
 DE cDNA encoding type 5 sodium channel protein designated PN5.

XX Type 5 sodium channel; PN5; nervous system; plexiform;
 KW dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;
 KW diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
 KW neuropathic pain; migraine; headache; ss.

XX
 OS Rattus sp.

XX
 PN FR2771103-A1.

XX
 PD 21-MAY-1999.

XX
 PF 19-NOV-1998; 98FR-0014551.

XX
 PR 20-NOV-1997; 97US-0066225.

FT mutation 1096
 FT /label= d
 FT /note= "Causes Ser > Phe substitution"
 FT 1984
 FT /tag= e
 FT /label= G>C
 FT 1965
 FT /tag= f
 FT /label= C>G
 FT /note= "Causes His > Asp substitution"
 FT 2472
 FT /tag= g
 FT /label= A>T
 FT /note= "Causes Thr > Ser substitution"
 FT 2986
 FT /tag= h
 FT /label= G>T
 FT /note= "Causes Ser > Ile substitution"
 FT 3019
 FT /tag= i
 FT /label= A>G
 FT /note= "Causes His > Arg substitution"
 FT 3158
 FT /tag= j
 FT /label= C>T
 FT 3525
 FT /tag= k
 FT /label= C>G
 FT /note= "Causes His > Asp substitution"
 FT 3556
 FT /tag= l
 FT /label= G>C
 FT /note= "Causes Arg > Thr substitution"
 FT 5893
 FT /tag= m
 FT /label= T>G
 FT /note= "Causes Ile > Ser substitution"
 FT 6525.6527
 FT /tag= n
 FT /note= "Addition of AAA"

XX WO9701577-A1.
 XX 16-JAN-1997.
 XX 25-JUN-1996; 96WO-GB01523.
 XX 28-JUN-1995; 95GB-0013180.
 XX (UNLO) UNIV COLLEGE LONDON.
 XX Akopian AN, Wood JN;
 XX WPI; 1997-100165/09.
 XX P-PSDB; AAW21740.
 XX
 PT New isolated mammalian sensory neuron sodium channel protein - used
 PT to identify modulators of the sodium channel, partic. for the
 PT treatment of pain
 XX
 PS Claim 9; Page 85-93; 128pp; English.
 XX
 CC The sequences given in AAT77803-06 encode the wild type and three
 CC variant forms of a rat sensory neuron sodium channel protein which
 CC is insensitive to tetrodotoxin. The proteins can be used for
 CC identifying modulators of the sodium channel. Blockers of the
 CC sodium channel will block or prevent the transmission of impulses
 CC along sensory neurons and thereby be useful in the treatment of acute,
 CC chronic or neuropathic pain. The novel protein is found only in sensory
 CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,
 CC enteric or central nervous system. The protein is found preferably in
 CC the neurons of the dorsal root ganglia or cranial ganglia. This

CC sequence contains 12 nucleotide differences to the wildtype rat
 CC DRG(SNS-B) (see also AAT77803) causing nine amino acid changes.
 XX
 SQ Sequence 6527 BP; 1542 A; 1863 C; 1663 G; 1459 T; 0 other;
 Query Match 12.8%; Score 38.4; DB 18; Length 6527;
 Best Local Similarity 62.5%; Pred. No. 0.035;
 Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 C 123 aattccgccccttcacttcgactctctgctgcaattgagaagcggttgccatccaa 182
 ||||| | | ||||| | | ||||| | | ||||| | ||||| ||
 D 237 aatttcagacggttcactccagatcactggtgagagatcgagagcagattgctgctac 296
 ||||| | | ||||| | | ||||| | | ||||| | ||||| ||
 Q 183 aaggagaaaaaagagtcttaagaccagacagagagaa 218
 || ||||| | | | || |||||
 D 297 cgggagccaagaaggccagaccagcaagcacagagga 332

RESULT 13

AAT77805

ID AAT77805 standard; cDNA; 7052 BP.

XX AC AAT77805;

XX UT 09-OCT-1997 (first entry)

XX DE cDNA encoding variant rat DRG (SNS-B) #2.

XX Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
 KW modulator; impulse; sensory neuron; acute pain; chronic pain;
 KW neuropathic pain; glia; muscle; parasympathetic nervous system;
 KW enteric nervous system; central nervous system; dorsal root ganglia;
 KW cranial ganglia; ss.

XX Rattus rattus.

XX Key Location/Qualifiers

XX CDS 204...6602

XX /tag= a

XX /product= Variant_Rat_DRG(SNS-B)

XX WO9701577-A1.

XX 16-JAN-1997.

XX 25-JUN-1996; 96WO-GB01523.

XX 28-JUN-1995; 95GB-0013180.

XX (UNLO) UNIV COLLEGE LONDON.

XX Akopian AN, Wood JN;

XX WPI; 1997-100165/09.

XX P-PSDB; AAW21739.

XX
 PT New isolated mammalian sensory neuron sodium channel protein - used
 PT to identify modulators of the sodium channel, partic. for the
 PT treatment of pain
 XX
 PS Claim 9; Page 69-78; 128pp; English.
 XX
 CC The sequences given in AAT77803-06 encode the wild type and three
 CC variant forms of a rat sensory neuron sodium channel protein which
 CC is insensitive to tetrodotoxin. The proteins can be used for
 CC identifying modulators of the sodium channel. Blockers of the
 CC sodium channel will block or prevent the transmission of impulses
 CC along sensory neurons and thereby be useful in the treatment of acute,
 CC chronic or neuropathic pain. The novel protein is found only in sensory
 CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,
 CC enteric or central nervous system. The protein is found preferably in
 CC the neurons of the dorsal root ganglia or cranial ganglia. This

CC sequence encodes a 2132 amino acid protein that contains a 176 amino
 CC acid repeat inserted after amino acid 585 of wildtype rat DRG(SNS-B)
 CC (see also AAW21737).

SQ Sequence 7052 BP; 1655 A; 2009 C; 1795 G; 1593 T; 0 other;

Query Match 12.8%; Score 38.4; DB 18; Length 7052;
 Best Local Similarity 62.5%; Pred. No. 0.036;
 Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Oy 123 aatttcgcccctcactccgactctgctgctgcaattgagaagcgattgccaacaa 182
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 Db 237 aatttcagaggttcactcccgagtcactgagcagatcgagaagcagattgctgtcac 296
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Oy 183 aaggagaaaagaagtctaaagaccagacagagagaa 218
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 297 cggcagcaagaaggccagaaccaagcacagagga 332

RESULT 14
 AAF57009 standard; cDNA; 6344 BP.

XX AAF57009;

DT 14-MAY-2001 (first entry)

XX Rat PN3 CDNA sequence.

XX Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;
 KW tetrodotoxin; TRX; peripheral nerve sodium channel type 3; PN3; rat;
 KW sodium channel protein; peripheral nervous system; allodynia; neuropathy;
 KW hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnerary;
 KW analgesic; anti-HIV; ss.

XX Rattus sp.

XX Key Location/Qualifiers
 FH 23..5893
 CDS /*tag= a
 FT /product= "PN3"

XX US6184349-B1.

XX 06-FEB-2001.

XX 15-APR-1997; 97US-0843417.

XX 11-OCT-1995; 95US-0511828.

XX (SYNT) SYNTEX USA INC.

PI Herman R, Delgado SG, Fish LM, Sangameswaran L, Robert DK;

XX WPI; 2001-202004/20.

DR P-PSDB; AAB61995.

PT New rat and human tetrodotoxin-resistant, voltage-gated sodium channel
 PT proteins, present in peripheral nerve tissue, useful as a therapeutic
 PT target for compounds treating peripheral nervous system disorders

PS Example 2; Fig 1A-I; 86pp; English.

XX The invention provides purified and isolated rat and human peripheral
 CC nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins.
 CC The rat peripheral nerve sodium channel type 3 (PN3) protein or its human
 CC homologue are useful for the development of antibodies against PN3 which
 CC are useful in affinity chromatography to purify recombinant sodium
 CC channel proteins or polypeptides, or as a research tool. The PN3 proteins
 CC are useful as therapeutic targets for compounds to treat disorders of the
 CC peripheral nervous system such as allodynia, hyperalgesia, diabetic
 CC neuropathy, traumatic injury and acquired immunodeficiency syndrome

CC (AIDS)-associated neuropathy. The present sequence represents the cDNA
 CC encoding the rat PN3 protein.

SQ Sequence 6344 BP; 1487 A; 1823 C; 1622 G; 1412 T; 0 other;

Query Match 12.6%; Score 37.8; DB 22; Length 6344;
 Best Local Similarity 57.7%; Pred. No. 0.053;
 Matches 94; Conservative 0; Mismatches 57; Indels 12; Gaps 1;

Oy 123 aatttcgcccctcactccgactctgctgctgcaattgagaagcgatt----- 173
 ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 56 aatttcagaggttcactcccgagtcactgagcagatcgagaagcagattgctgtcac 115
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Oy 174 ---gcattcccaaaagagaaaagaagtctaaagaccagacagagagaagtaaccagacct 230
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 116 cgcgcagcaagaagccagaaccaagcacagagacagagagacaaagcgagagagccc 175
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Oy 231 caactcagcttgacctaaaggctccagggaagtgcaccaact 273
 ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 176 aggcctcagctggacttgaaagcctgtaaccagctgccaagt 218

RESULT 15

AAAT77803

DT AAT77803 standard; cDNA; 6524 BP.

XX AAT77803;

XX 09-OCT-1997 (first entry)

XX CDNA encoding wild type rat DRG (SNS-B).

Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
 KW modulator; impulse; sensory neuron; acute pain; chronic pain;
 KW neuropathic pain; glia; muscle; parasympathetic nervous system;
 KW enteric nervous system; central nervous system; dorsal root ganglia;
 KW cranial ganglia; ss.

XX Rattus rattus.

XX Key Location/Qualifiers
 FH 204..6077
 CDS /*tag= a
 FT /product= Rat_DRG(SNS-B)

XX WO9701577-A1.

XX 16-JAN-1997.

XX 25-JUN-1996; 96WO-GB01523.

XX 28-JUN-1995; 95GB-0013180.

XX (UNLO) UNIV COLLEGE LONDON.

PI Akopian AN, Wood JN;

XX WPI; 1997-100165/09.

DR P-PSDB; AAW21737.

PT New isolated mammalian sensory neuron sodium channel protein - used
 PT to identify modulators of the sodium channel, partic. for the
 PT treatment of pain

PS Claim 9; Page 50-58; 128pp; English.

XX The sequences given in AAT77803-06 encode the wild type and three
 CC variant forms of a rat sensory neuron sodium channel protein which
 CC is insensitive to tetrodotoxin. The proteins can be used for
 CC identifying modulators of the sodium channel. Blockers of the
 CC sodium channel will block or prevent the transmission of impulses
 CC along sensory neurons and thereby be useful in the treatment of acute,

CC chronic or neuropathic pain. The novel protein is found only in sensory
 CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,
 CC enteric or central nervous system. The protein is found preferably in
 CC the neurons of the dorsal root ganglia or cranial ganglia.

xx
 SQ Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T; 0 other;

Query Match 12.38; Score 36.8; DB 18; Length 6524;
 Best Local Similarity 61.58; Pred. No. 0.11;
 Matches 59; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 123 aatttcgccccttcaactccgactctctggtgctgaattgagaagcggttgccatcaa 182
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Db 237 aatttcagacggttcactccagagtcactgacagagatcgagaagcagattgtgtctcac 296
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Qy 183 aaggagaaaaaagtcttaagaccagacagagagaa 218
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Db 297 cgcgagccaagaaggccagaaccaagcacagagga 332
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Search completed: February 26, 2002, 22:49:53
 Job time: 15273 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 22:39:38 ; Search time 177.56 Seconds
(without alignments)
381.375 Million cell updates/sec

Title: US-09-646-224A-3
Perfect score: 299
Sequence: 1 atctaggcaggctgtttt.....cgacaatctcggaggcttt 299

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued_Patents_NA.*
- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
 - 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
 - 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
 - 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
 - 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	45.8	15.3	5874	4	US-08-843-417-9	Sequence 9, Appli
2	37.8	12.6	6344	4	US-08-843-417-1	Sequence 1, Appli
3	30.4	10.2	5461	3	US-07-998-289B-7	Sequence 7, Appli
4	30.4	10.2	6513	1	US-08-338-702-7	Sequence 7, Appli
5	30.4	10.2	6513	1	US-08-337-339-7	Sequence 7, Appli
6	30.4	10.2	6513	1	US-08-724-095-7	Sequence 7, Appli
7	30.4	10.2	6513	5	PCT-US95-14262-7	Sequence 7, Appli
8	30.4	10.2	6513	5	PCT-US95-14378-7	Sequence 7, Appli
9	30.4	10.2	6519	2	US-08-808-793-24	Sequence 24, Appl
10	29	9.7	767	4	US-08-998-416-566	Sequence 24, Appl
11	28.8	9.6	6315	2	US-08-808-793-2	Sequence 2, Appli
12	28.8	9.6	6315	3	US-08-772-512A-2	Sequence 2, Appli
13	28.8	9.6	6318	2	US-08-808-793-1	Sequence 1, Appli
14	28.8	9.6	6318	3	US-08-772-512A-1	Sequence 1, Appli
15	28.6	9.6	2174	2	US-08-665-040-1	Sequence 1, Appli
16	28.4	9.5	6452	3	US-08-836-325-9	Sequence 9, Appli
17	28.2	9.4	9370	1	US-08-320-559-27	Sequence 27, Appl
18	28.2	9.4	9370	3	US-08-545-860D-27	Sequence 27, Appl
19	28.2	9.4	9370	5	PCT-US94-04496-27	Sequence 27, Appl
20	28.2	9.4	9391	1	US-08-320-559-25	Sequence 25, Appl
21	28.2	9.4	9391	3	US-08-545-860D-25	Sequence 25, Appl
22	28.2	9.4	9391	5	PCT-US94-04496-25	Sequence 25, Appl
23	28	9.4	434	3	US-08-581-918A-33	Sequence 33, Appl
24	28	9.4	434	4	US-08-346-147B-33	Sequence 33, Appl
25	28	9.4	823	4	US-08-998-416-505	Sequence 505, App
26	28	9.4	1647	1	US-08-198-446B-9	Sequence 9, Appli
27	28	9.4	1647	2	US-08-870-693-9	Sequence 9, Appli

28	28	9.4	2809	1	US-08-484-105-3	Sequence 3, Appli
29	28	9.4	2809	1	US-08-484-106-3	Sequence 3, Appli
30	28	9.4	4237	1	US-07-844-298B-1	Sequence 1, Appli
31	27.8	9.3	1025	4	US-08-643-212-19	Sequence 19, Appl
32	27.8	9.3	1025	4	US-08-643-212-23	Sequence 23, Appl
33	27.8	9.3	1995	1	US-08-425-069-3	Sequence 3, Appli
34	27.8	9.3	1995	2	US-08-317-844B-3	Sequence 3, Appli
35	27.8	9.3	5977	3	US-09-024-020B-1	Sequence 1, Appli
36	27.8	9.3	6007	3	US-09-024-020B-2	Sequence 2, Appli
37	27.8	9.3	6556	3	US-09-024-020B-7	Sequence 7, Appli
38	27.8	9.3	6586	3	US-09-024-020B-43	Sequence 43, Appl
39	27.8	9.3	6826	3	US-09-024-020B-8	Sequence 8, Appli
40	27.6	9.2	1490	4	US-09-197-679A-2	Sequence 2, Appli
41	27.2	9.1	2369	4	US-08-910-925-2	Sequence 2, Appli
42	27.2	9.1	5707	2	US-08-472-809B-8	Sequence 8, Appli
43	27.2	9.1	6345	2	US-08-472-809B-7	Sequence 7, Appli
44	27.2	9.1	9103	1	US-08-466-033-182	Sequence 182, App
45	27.2	9.1	9103	1	US-08-444-733-182	Sequence 182, App

ALIGNMENTS

RESULT 1
US-08-843-417-9
Sequence 9, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843.417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5874 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-843-417-9

Query Match 15.3%; Score 45.8; DB 4; Length 5874;
Best Local Similarity 60.7%; Pred. No. 4.6e-06;

GENERAL INFORMATION:
APPLICANT: Warmke, Jeffrey W.
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/338,702
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-338-702-7

Query Match 10.2%; Score 30.4; DB 1; Length 6513;
Best Local Similarity 63.9%; Pred. No. 1.3;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 126 ttccgccccttcaacttcgactctctgctgcaattgagaagcgattgccaataaag 185
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Db 69 TTCCGTCCTTTACCCGCGAATCTTGGTCAAAATCGAACACGATTGCCGCTCAACAT 128
Qy 186 gagaaaaaagaag 197
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Db 129 GAAAGCAGAG 140

RESULT 5
US-08-337-339-7
Sequence 7, Application US/08337339
Patent No. 5593864
GENERAL INFORMATION:
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Hall, Linda
APPLICANT: Feng, Gouping
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/337,339
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19332
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-337-339-7

Query Match 10.2%; Score 30.4; DB 1; Length 6513;
Best Local Similarity 63.9%; Pred. No. 1.3;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Db 69 TTCCGTCCTTTACCCGCGAATCTTGGTCAAAATCGAACACGATTGCCGCTCAACAT 128
Qy 186 gagaaaaaagaag 197
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Db 129 GAAAGCAGAG 140

RESULT 6
US-08-724-095-7
Sequence 7, Application US/08724095
Patent No. 5688917
GENERAL INFORMATION:
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Hall, Linda
APPLICANT: Feng, Gouping
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
STREET: P.O. Box 2000 - 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTseq, Version #1.d5
CURRENT APPLICATION DATA: US/08/724,095
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19332DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:

Query Match 9.7%; Score 29; DB 4; Length 767;

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DB	157	GCACTACATGCCACTGGCGCATCTATGGGATGTGCTCTACAGAAGGAATACAACTGCTAT	216
QY	179	ccaaaaggagaaaagaagtcttaaaagccagacagcaggagaagtaccgccagcctcaacctca	238
DB	217	TCCAAAGAATTCGACGTTGTGCATGCCAAGAACCTGCAGAAACAAGGCGAAGACGAA	276
QY	239	gcttgacctaaaggcctccaggag	263
DB	277	GGTTTCAGTTCAATACGTTGCTGAAG	301

RESULT 11
US-08-808-793-2
Sequence 2, Application US/08808793
Patent No. 5858713
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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Query Match          9.6%; Score 28.8; DB 3; Length 6315;
Best Local Similarity 52.5%; Pred. No. 4.8;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
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RESULT 13
US-08-808-793-1

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,793

FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: US 60/034,361
 FILING DATE: 24-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/012,649
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Braman, Susan J.
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 716-263-1636
 TELEFAX: 716-263-1600


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; FEATURE:
; NAME/KEY: untranslated 5'
; LOCATION: 1..48
; FEATURE:
; NAME/KEY: coding sequence
; LOCATION: 49..560
; OTHER INFORMATION: Down Syndrome critical region 1 (DSCR1)
; FEATURE:
; NAME/KEY: DSCR1
; LOCATION: 1..171 PEPTIDES
; IDENTIFICATION METHOD: translation of the DSCR1 sequence.
; OTHER INFORMATION:
; OTHER INFORMATION: - deduced protein
; OTHER INFORMATION: - proline-rich protein domains
; OTHER INFORMATION: - glutamic acid-rich protein domains
; OTHER INFORMATION: - leucine/phenylalanine-rich protein domains
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; NAME/KEY: untranslated 3'
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; LOCATION: 1541..1546 AND 2132..2137
; US-08-665-040-1

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Best Local Similarity 59.0%; Pred. No. 3.1;
Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy 252 gcctccaggaagttgccaaactc 274
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Db 573 GCGACGAGGAGCGCATTCCAAATC 595

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Search completed: February 26, 2002, 22:39:47
 Job time: 17247 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 20:07:03 ; Search time 5057.4 Seconds
(without alignments)
635.304 Million cell updates/sec

Title: US-09-646-224A-3
Perfect score: 299
Sequence: 1 atcctaggcagcggtgtttt.....cgacaatcctcgaggcttt 299

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:
1: em_estfun:
2: em_esthum:
3: em_estin:
4: em_estom:
5: em_estpl:
6: em_estba:
7: em_estro:
8: em_estov:
9: em_htc:
10: gb_estl:
11: gb_est2:
12: gb_htc:
13: gb_gss:
14: em_gss_fun:
15: em_gss_hum:
16: em_gss_inv:
17: em_gss_pln:
18: em_gss_pro:
19: em_gss_rod:
20: em_gss_vrt:
21: em_gss_other:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	39	13.0	491	11	BF600973	MA
2	39	13.0	493	11	BF706700	MA
3	39	13.0	504	10	BE485569	BA
4	39	13.0	532	10	BE752960	MA
5	39	13.0	533	10	AW654550	MA
6	35.2	11.8	366	10	BE685650	x
7	35.2	11.8	885	13	AQ739595	HS_5381_B
8	34.6	11.6	400	11	BG663266	DRAAGA02
9	34.6	11.6	581	10	BE251756	MA
10	34.2	11.4	515	10	AV668453	MA
11	34	11.4	407	10	AA134408	z026c11.r
12	33.8	11.3	504	13	AZ017956	RPCI-23-2

13	33.8	11.3	684	10	AL594553	AL594553
14	33.6	11.2	386	10	BE632098	uu56h06.y
15	33.4	11.2	591	13	AQ727308	HS_5435_B
16	33.2	11.1	289	10	BA451462	BA451462
17	33.2	11.1	546	10	AA544829	yj69f10.r
18	33.2	11.1	1101	13	CNS016NJ	AL108969 Drosophil
19	33	11.0	426	10	AW365859	MRO-HT007
20	33	11.0	437	10	AW365809	MRO-HT007
21	33	11.0	462	11	BE816689	RC5-BN023
22	33	11.0	676	10	AU170796	AU170796
23	33	11.0	695	10	BE053445	GA_Ea000
24	33	11.0	830	13	CNS03VOW	AL262697 Tetraodon
25	33	11.0	838	11	BF631471	HVSMED001
26	33	11.0	911	11	BG443355	GA_Ea002
27	33	11.0	912	11	BG443355	GA_Ea002
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29	32.8	11.0	586	10	AU204804	AU204804
30	32.6	10.9	260	10	AI527318	u345906.x
31	32.6	10.9	443	10	AW214225	u045a07.x
32	32.6	10.9	498	13	AZ288737	RPCI-23-1
33	32.6	10.9	674	13	AQ391592	CITBI-E1-
34	32.6	10.9	910	13	CNS05PAI	AL347715 Tetraodon
35	32.6	10.9	967	11	BF571561	BF571561 602078169
36	32.4	10.8	361	11	BF232577	des1c02.x
37	32.4	10.8	392	10	AW804539	QVO-UM009
38	32.2	10.8	327	13	AZ843152	2M0141G20
39	32.2	10.8	367	11	BG408173	de69a02.x
40	32.2	10.8	443	10	AA982787	uh15f04.r
41	32.2	10.8	514	11	BG019419	dab08901.
42	32.2	10.8	522	11	BG486913	dc99f11.x
43	32.2	10.8	595	11	EG555371	de94e11.x
44	32.2	10.8	597	10	AW351192	GM210010B
45	32.2	10.8	618	10	AW460583	da26c06.x

ALIGNMENTS

RESULT 1
BF600973 1
LOCUS 265816 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF600973
ACCESSION BF600973
VERSION BF600973.1 GI:11698194
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 491)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C., Bennett
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
Pertege,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine CDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
COMMENT 21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTGCTACGAG
Plate: 39 row: K column: 13


```

Db 62 GGGAGATGGAGCACAGGTTCTCTTGCTGCTGCTGCCCTTCTCTCCCAAG 121
Qy 147 tctctggctgaattgagaagcg 169
Db 122 TGAATCCCGCATCTTAAAGTG 144

RESULT 6
LOCUS BE685650 366 bp mRNA EST 11-SEP-2000
DEFINITION uu56h06.x1 Soares_thymus_2NbMT Mus musculus cDNA clone
ACCESSION IMAGE:3375995 3', mRNA sequence.
VERSION BE685650
KEYWORDS BE685650.1 GI:10073326
SOURCE EST.
ORGANISM house mouse.
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 366)
COMMENT NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: crapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1085599
High quality sequence stop: 348.
FEATURES
Location/Qualifiers
Source
1..366
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3375995"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TCTTACCAACTGAGTGGAGGCGCGGTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 144 a 56 c 114 g 52 t
ORIGIN
Query Match 11.8%; Score 35.2; DB 10; Length 366;
Best Local Similarity 52.08; Pred. No. 12;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 67 tcttgaggtgaagatgacagatgctaccagtaattcttccagatgagcggaatt 126
Db 149 TCCGAGGCGGAGGAGGAGGATCAAGAGTTCAAAGTCATCTTCAGCTACAAATGAAGTT 208
Qy 127 tccgccccttcaactccgactctctgctgcaattgagaagcgattgccatccaaagg 186
Db 209 GGAGACCAATCAGACCCCTCTCAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGG 268
Qy 187 agaaaaaagagctcaagaccagcagagagaa 218
Db 269 AGGGGAGACCCGATTAAGAGGAGGAGGAGGA 300

```

```

RESULT 7
LOCUS AQ739595 885 bp DNA GSS 16-JUL-1999
DEFINITION HS_5381_B2_H01_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=957 Col=2 Row=P, DNA sequence.
ACCESSION AQ739595
VERSION AQ739595.1 GI:5517117
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 885)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 957 row: P column: 2
Seq primer: T7
Class: BAC ends
High quality sequence stop: 885.
FEATURES
Location/Qualifiers
Source
1..885
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=957 Col=2 Row=P"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"
BASE COUNT 193 a 169 c 183 g 331 t 9 others
ORIGIN
Query Match 11.8%; Score 35.2; DB 13; Length 885;
Best Local Similarity 48.6%; Pred. No. 13;
Matches 85; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 71 gaggggtgaagatgacagatgctaccagtaattcttccagatgagcggaattccg 130
Db 638 GAGGTTGAGGCGAGGAGATCTCTTTGAACCCAGGAGGAGGTTTGCAGTGACCCGAGATAGCG 579
Qy 131 cccctcaacttccgactctctgctgcaattgagaagcgattgccatcccaaaaggagaa 190
Db 578 CCCCTGCACTCCAGCTGGGAGAGGACAGGCAAAACAAAGTCTCCCCNNAANAAAAA 519
Qy 191 aaagaagtctaaagaccagacagaggaagtagtaccagcctcaaacctcagctgac 245
Db 518 AAAAAAANNAANNAANNAANNAAGNNGGTTATACACCACCAAGTCAATTTAAC 464

RESULT 8
BGG63266

```


JOURNAL
COMMENT

Unpublished (2000)
Contact: Kiyoshi Naruse
Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Sugano-Kawakami 5' end enriched cDNA library (OLA).

FEATURES

source
Location/Qualifiers
1. 515
/organism="Oryzias latipes"
/strain="HNI"
/db_xref="taxon:8090"
/clone="OLA03.01f"
/clone_lib="Sugano Kawakami 5' enriched cDNA library (OLA)"
/tissue_type="whole body"
/dev_stage="adult"
BASE COUNT 135 a 152 c 108 g 115 t 5 others
ORIGIN

Query Match 11.4%; Score 34.2; DB 10; Length 515;
Best Local Similarity 48.2%; Pred. No. 24;
Matches 96; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 12 ggcgtttttatccgcctctgagccctctctgaggtatgtggtgtgtctgtctgtcgtg 71
Db 25i GGTTCCTTCAATCAACCATCACAGCGCTCATGTCTCAACACAGAGCGCTCTGGCCCTCTG 310
QY 72 aggggtgaagatggatgacagatgctaccacagtaatactttccagatgacggaatttcgcg 131
Db 311 AACCTGGAGATCGACCCCAATATTCAGACTGTCCGCCACCCAGGAGAGACGACATCAAG 370
QY 132 ccttctactctccgactctctgctgcaattgagaagcggattgcatcccaaaaggagaaa 191
Db 371 TCCCTCAACAACCGCTTTCGCGACTTTCATCGACAAGGTCCTTCTCGGACGACGAGAAC 430
QY 192 aagaagtctaagaccaga 210
Db 431 AAGATGCTTGGAGACCAAAA 449

RESULT 11

AA134408
LOCUS
DEFINITION 2026cll.11 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:588020 5', mRNA sequence.
AA134408
ACCESSION
VERSION AA134408.1 GI:1692033
KEYWORDS
SOURCE EST.
human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 407)

REFERENCE

AUTHORS
Hillier, B., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., DuBuque, T., Favell, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

TITLE

JOURNAL
MEDLINE
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 840 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 385.

FEATURES

source
Location/Qualifiers
1. 407
/organism="Homo sapiens"
/db_xref="GDB:4620322"
/db_xref="taxon:9606"
/clone="IMAGE:588020"
/clone_lib="Stratagene colon (#937204)"
/tissue_type="tumor"
/cell_line="H84 carcinoma cell line"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site: 1:
EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATCGCGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTTCTTTT 3"
BASE COUNT 85 a 116 c 137 g 64 t 5 others
ORIGIN

Query Match 11.4%; Score 34; DB 10; Length 407;
Best Local Similarity 61.9%; Pred. No. 27;
Matches 52; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 11 aggggtttttatccgcctctctgagccctctctgaggtatgtggtgtgtctgtctgtcct 70
Db 217 AAGATGTTTATTTTCAACCCACCTGACTGTTCCACACACCAAGCCCTGTGCTGCCCT 276

QY 71 gagggtgaagatggatgacagatg 94
Db 277 TGAGGGAAGTGTGTTGANCCTTG 300

RESULT 12

AA2017956
LOCUS
DEFINITION AA2017956.1 TV RPCI-23 Mus musculus genomic clone RPCI-23-259K13
IMAGE:588020 5', DNA sequence.
AA2017956
ACCESSION
VERSION AA2017956.1 GI:7093340
KEYWORDS
SOURCE GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 504)

REFERENCE

AUTHORS
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret,
B., Levins, M., Megann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)

TITLE

JOURNAL
COMMENT
Other_GSSs: RPCI-23-259K13.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@ejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 259 row: K column: 13
Seq primer: T7
Class: BAC ends.

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